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OM protein - protein search, using sw model

Run on: June 24, 2004, 15:18:25 ; Search time 50 seconds
(without alignments)
4584.774 Million cell updates/sec

Title: US-09-873-409-2
Perfect score: 4079
Sequence: 1 MVDENDIRALNVHRDHIG.....QELLNRDIYFKLVNAQSVQ 812

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	4079	100.0	812	US-09-873-409-2
2	4079	100.0	1058	US-09-873-409-4
3	4079	100.0	1195	US-09-873-409-6
4	4079	100.0	1222	US-09-873-409-5
5	3919	96.1	1232	US-10-415-378-14
6	3323	81.5	659	US-09-873-409-1
7	3188.5	77.7	1354	US-10-092-900A-304
8	2465.5	60.4	1066	US-09-817-762-5
9	2465.5	60.4	1275	US-10-363-112-49
10	2442	59.9	1281	US-10-101-433A-7
11	2442	59.9	1281	US-10-101-433A-8
12	2442	59.9	1281	US-10-101-433A-9
13	2441	59.8	1272	US-09-769-097-2
14	2441	59.8	1272	US-09-769-097-4
15	2441	59.8	1280	US-10-101-433A-3

Sequence 2, Appli	16	2441	59.8	1280	16	US-10-619-359A-2
Sequence 10, Appli	17	2441	59.8	1281	14	US-10-101-433A-10
Sequence 2, Appli	18	2441	59.8	1283	14	US-10-101-433A-2
Sequence 4, Appli	19	2441	59.8	1283	14	US-10-101-433A-4
Sequence 2, Appli	20	2441	59.8	1283	16	US-10-619-359A-4
Sequence 11, Appli	21	2438	59.8	1280	13	US-10-044-671-2
Sequence 7, Appli	22	2438	59.8	1280	14	US-10-101-433A-11
Sequence 15, Appli	23	2438	59.8	1280	16	US-10-619-359A-7
Sequence 10, Appli	24	2438	59.8	1280	16	US-10-343-657-15
Sequence 17, Appli	25	2437	59.7	1280	16	US-10-343-657-10
Sequence 6, Appli	26	2436	59.7	1278	12	US-09-805-020-66
Sequence 6, Appli	27	2436	59.7	1279	14	US-10-097-340-2
Sequence 2, Appli	28	2436	59.7	1279	14	US-10-101-433A-6
Sequence 4, Appli	29	2436	59.7	1279	16	US-10-619-359A-6
Sequence 2, Appli	30	2436	59.7	1280	9	US-09-866-866A-2
Sequence 3, Appli	31	2436	59.7	1280	9	US-09-866-866A-4
Sequence 7, Appli	32	2436	59.7	1280	12	US-09-817-762-3
Sequence 5, Appli	33	2436	59.7	1280	13	US-10-072-621-7
Sequence 5, Appli	34	2436	59.7	1280	14	US-10-101-433A-5
Sequence 2, Appli	35	2436	59.7	1280	16	US-10-619-359A-5
Sequence 3, Appli	36	2436	59.7	1280	16	US-10-343-657-2
Sequence 4, Appli	37	2436	59.7	1280	16	US-10-343-657-3
Sequence 5, Appli	38	2436	59.7	1280	16	US-10-343-657-4
Sequence 6, Appli	39	2436	59.7	1280	16	US-10-343-657-5
Sequence 9, Appli	40	2436	59.7	1280	16	US-10-343-657-6
Sequence 12, Appli	41	2436	59.7	1280	16	US-10-343-657-9
Sequence 13, Appli	42	2436	59.7	1280	16	US-10-343-657-12
Sequence 14, Appli	43	2436	59.7	1280	16	US-10-343-657-13
	44	2436	59.7	1280	16	US-10-343-657-14
	45	2436	59.7	1280	16	US-10-343-657-14

ALIGNMENTS

RESULT 1
US-09-873-409-2
; Sequence 2, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/368611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-873-409-2

Query Match	100.0%;	Score 4079;	DB 9;	Length 812;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 812;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	MVDENDIRALNVHRDHIGVWSQEPVLTGTTISNNIKYGRDDVTDEEMERAAAREANAYD	60	
Db	1	MVDENDIRALNVHRDHIGVWSQEPVLTGTTISNNIKYGRDDVTDEEMERAAAREANAYD	60	
QY	61	FIMEFFNKFTLVGKGAQMSGGQKQRIARALVKNPKILILDEATSAIDSEKSAVQA	120	
Db	61	FIMEFFNKFTLVGKGAQMSGGQKQRIARALVKNPKILILDEATSAIDSEKSAVQA	120	
QY	121	ALEKASGKTTIVVHRLSTIRSADLIVTKQGLAEKGAHAELMAKRGLYVSLVMSQDI	180	
Db	121	ALEKASGKTTIVVHRLSTIRSADLIVTKQGLAEKGAHAELMAKRGLYVSLVMSQDI	180	
QY	181	KKADEQMSMTYSTERKTNLPLHSVKSIKSDFDIKAEESTQSKISLPEVSLKILKLN	240	

US-09-873-409-6

Query Match 100.0%; Score 4079; DB 9; Length 1195;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYDENIRALNVHRHVDHIGVVSQEPVLFQTTISNNIKYGRDDVTDDEMERAAAREANAYD 60
DB 384 MYDENIRALNVHRHVDHIGVVSQEPVLFQTTISNNIKYGRDDVTDDEMERAAAREANAYD 443

QY 61 FINEFPNKFNTLVGEGKQMSGGQKQRIARALVRNPKILILDEATSDALDSKSAVQA 120
DB 444 FINEFPNKFNTLVGEGKQMSGGQKQRIARALVRNPKILILDEATSDALDSKSAVQA 503

QY 121 ALEKASKGRTTIVVAHRLSTIRSAOLIVTLKQMLAEKGAHAELMAKRGLYYSLVMSQDI 180
DB 504 ALEKASKGRTTIVVAHRLSTIRSAOLIVTLKQMLAEKGAHAELMAKRGLYYSLVMSQDI 563

QY 181 KKADQWESMTYSTERTKNSLPHSVKSIKSDPIDKABESTQSKBISLPEVSLKILKLN 240
DB 564 KKADQWESMTYSTERTKNSLPHSVKSIKSDPIDKABESTQSKBISLPEVSLKILKLN 623

QY 241 KPWPFPVLGTASVLNGTVHPVFSIIFAKIITMFGNNDKTTILKHDAEYYSIMFVILGVI 300
DB 624 KPWPFPVLGTASVLNGTVHPVFSIIFAKIITMFGNNDKTTILKHDAEYYSIMFVILGVI 683

QY 301 CPVSYFMQGLFYGRAGEILTMRLHLAFKAMLYQDIAMFDEKENSTGGTTLAIDIAQI 360
DB 684 CPVSYFMQGLFYGRAGEILTMRLHLAFKAMLYQDIAMFDEKENSTGGTTLAIDIAQI 743

QY 361 QGATGSRIGVLTQNTNMGSLVSIISFYGWEMTFLILSIAPVLAVTGMETAAVTGFANK 420
DB 744 QGATGSRIGVLTQNTNMGSLVSIISFYGWEMTFLILSIAPVLAVTGMETAAVTGFANK 803

QY 421 DKQELKHAGKIATEALENIRITVSLTREKAFQOMYEMLOTOHRNTSKKAQIIGSCYAFS 480
DB 804 DKQELKHAGKIATEALENIRITVSLTREKAFQOMYEMLOTOHRNTSKKAQIIGSCYAFS 863

QY 481 HAFIYFAYAAAGFRGAYLTOAGRMTPBGMFIVFTTAIYAGAMAIGKTLVLAPEYSKAKSGA 540
DB 864 HAFIYFAYAAAGFRGAYLTOAGRMTPBGMFIVFTTAIYAGAMAIGKTLVLAPEYSKAKSGA 923

QY 541 AHLFALLEKKPNIDSRQSGKPDTCBGNLFPREVSPFPCRPDVFILRGLSLSTERGKT 600
DB 924 AHLFALLEKKPNIDSRQSGKPDTCBGNLFPREVSPFPCRPDVFILRGLSLSTERGKT 983

QY 601 VAFVSGSGCKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQLRSQIAIVPQEPVLNC 660
DB 984 VAFVSGSGCKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQLRSQIAIVPQEPVLNC 1043

QY 661 SIAENIAYGDNRSRVPLDEIKEAANAANIHSFIEGLPEKYNTOVGLKGAQLSGGQKORLA 720
DB 1044 SIAENIAYGDNRSRVPLDEIKEAANAANIHSFIEGLPEKYNTOVGLKGAQLSGGQKORLA 1103

QY 721 IARALLQKPKILLDEATSDALDSKSAVQA 812
DB 1104 IARALLQKPKILLDEATSDALDSKSAVQA 1163

QY 781 LHNGKIKQGTQHQELLNRDIIYFKLVNAQSVQ 812
DB 1164 LHNGKIKQGTQHQELLNRDIIYFKLVNAQSVQ 1195

RESULT 4

US-09-873-409-5
; Sequence 5, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611

CURRENT APPLICATION NUMBER: US/09/873,409
CURRENT FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 1222
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: NO. US20020037522A1e
LOCATION: (230)..(230)
OTHER INFORMATION: Xaa at position 230 represents any L amino acid
US-09-873-409-5

Query Match 100.0%; Score 4079; DB 9; Length 1222;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYDENIRALNVHRHVDHIGVVSQEPVLFQTTISNNIKYGRDDVTDDEMERAAAREANAYD 60
DB 411 MYDENIRALNVHRHVDHIGVVSQEPVLFQTTISNNIKYGRDDVTDDEMERAAAREANAYD 470

QY 61 FIMEFPNKFNTLVGEGKQMSGGQKQRIARALVRNPKILILDEATSDALDSKSAVQA 120
DB 471 FIMEFPNKFNTLVGEGKQMSGGQKQRIARALVRNPKILILDEATSDALDSKSAVQA 530

QY 121 ALEKASKGRTTIVVAHRLSTIRSAOLIVTLKQMLAEKGAHAELMAKRGLYYSLVMSQDI 180
DB 531 ALEKASKGRTTIVVAHRLSTIRSAOLIVTLKQMLAEKGAHAELMAKRGLYYSLVMSQDI 590

QY 181 KKADQWESMTYSTERTKNSLPHSVKSIKSDPIDKABESTQSKBISLPEVSLKILKLN 240
DB 591 KKADQWESMTYSTERTKNSLPHSVKSIKSDPIDKABESTQSKBISLPEVSLKILKLN 650

QY 241 KPWPFPVLGTASVLNGTVHPVFSIIFAKIITMFGNNDKTTILKHDAEYYSIMFVILGVI 300
DB 651 KPWPFPVLGTASVLNGTVHPVFSIIFAKIITMFGNNDKTTILKHDAEYYSIMFVILGVI 710

QY 301 CPVSYFMQGLFYGRAGEILTMRLHLAFKAMLYQDIAMFDEKENSTGGTTLAIDIAQI 360
DB 711 CPVSYFMQGLFYGRAGEILTMRLHLAFKAMLYQDIAMFDEKENSTGGTTLAIDIAQI 770

QY 361 QGATGSRIGVLTQNTNMGSLVSIISFYGWEMTFLILSIAPVLAVTGMETAAVTGFANK 420
DB 771 QGATGSRIGVLTQNTNMGSLVSIISFYGWEMTFLILSIAPVLAVTGMETAAVTGFANK 830

QY 421 DKQELKHAGKIATEALENIRITVSLTREKAFQOMYEMLOTOHRNTSKKAQIIGSCYAFS 480
DB 831 DKQELKHAGKIATEALENIRITVSLTREKAFQOMYEMLOTOHRNTSKKAQIIGSCYAFS 890

QY 481 HAFIYFAYAAAGFRGAYLTOAGRMTPBGMFIVFTTAIYAGAMAIGKTLVLAPEYSKAKSGA 540
DB 891 HAFIYFAYAAAGFRGAYLTOAGRMTPBGMFIVFTTAIYAGAMAIGKTLVLAPEYSKAKSGA 950

QY 541 AHLFALLEKKPNIDSRQSGKPDTCBGNLFPREVSPFPCRPDVFILRGLSLSTERGKT 600
DB 951 AHLFALLEKKPNIDSRQSGKPDTCBGNLFPREVSPFPCRPDVFILRGLSLSTERGKT 1010

QY 601 VAFVSGSGCKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQLRSQIAIVPQEPVLNC 660
DB 1011 VAFVSGSGCKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQLRSQIAIVPQEPVLNC 1070

QY 661 SIAENIAYGDNRSRVPLDEIKEAANAANIHSFIEGLPEKYNTOVGLKGAQLSGGQKORLA 720
DB 1071 SIAENIAYGDNRSRVPLDEIKEAANAANIHSFIEGLPEKYNTOVGLKGAQLSGGQKORLA 1130

QY 721 IARALLQKPKILLDEATSDALDSKSAVQA 812
DB 1131 IARALLQKPKILLDEATSDALDSKSAVQA 1190

QY 781 LHNGKIKQGTQHQELLNRDIIYFKLVNAQSVQ 812
DB 1191 LHNGKIKQGTQHQELLNRDIIYFKLVNAQSVQ 1222

RESULT 5

US-10-415-378-14
; Sequence 14, Application US/10415378
; Publication No. US20040014945A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, V. Tom
; APPLICANT: YUE, Henry; NGUYEN, Daniel B.;
; APPLICANT: HAFALIA, April J.A.; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; CHAWLA, Narinder K.;
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.;
; APPLICANT: GANDHI, Ameena R.; DING, Li;
; APPLICANT: SANTANWALA, Madhundan M.; RAMKUNAR, Javalaxmi;
; APPLICANT: ARVIZU, Chandra S.; GIEZEN, Kimberly J.;
; APPLICANT: LAL, Frecci G.; AZIMZAI, Faida;
; APPLICANT: KHAN, Farrah A.; THANGAVELOU, Kavitha;
; APPLICANT: THORNTON, Michael B.; LU, Dyrung Aina M.;
; APPLICANT: TRIBOULEY, Catherine M.; WARREN, Bridget A.;
; APPLICANT: ISON, H. Craig; DAS, Debopriya;
; APPLICANT: RAUMANN, Brigitte E.; POLICKY, Jennifer L.;
; APPLICANT: KEARNEY, Liam
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0276 USN
; CURRENT APPLICATION NUMBER: US/10/415,378
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: PCT/US01/46055
; PRIOR FILING DATE: 2001-10-27
; PRIOR APPLICATION NUMBER: US 60/250,790
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/252,232
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/249,661
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/247,673
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,904
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/243,989
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 14
; LENGTH: 1232
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040014945A1 7472030CD1
US-10-415-378-14

Query Match 96.1%; Score 3319; DB 15; Length 1232;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 785; Conservative 1; Mismatches 0; Indels 26; Gaps 1;

QY 1 MVDENDIRALNVRYRDHIGVVSQEPVLFGTISNNIKYGRDDVTDEMERAREANAYD 60
DB 447 MVDENDIRALNVRYRDHIGVVSQEPVLFGTISNNIKYGRDDVTDEMERAREANAYD 506
QY 61 FIMEPPNFKNTLVGKGAQMGSGGQKQRIARALVRNPXKILILDEATSALDSSEKSAVQA 120
DB 507 FIMEPPNFKNTLVGKGAQMGSGGQKQRIARALVRNPXKILILDEATSALDSSEKSAVQA 566
QY 121 ALEKASKRTTIVVAHRLSTRSADLIIVTLKQGLAEKGAHAEKMAKRGLYSLVMSQDI 180
DB 567 ALEKASKRTTIVVAHRLSTRSADLIIVTLKQGLAEKGAHAEKMAKRGLYSLVMSQDI 626
QY 181 KKADEQMSMTYSTERTKNSPLHSVKSISKDFIDKABESTOSKEISLPEVSLKILKLN 240
DB 627 KKADEQMSMTYSTERTKNSPLHSVKSISKDFIDKABESTOSKEISLPEVSLKILKLN 686
QY 241 KEPEFVVLGTLASVLNGTVHPVFSIIIPAKIITMFGNNDKTTLKHDAEIYSMIFVLGVI 300

DB 687 KEPEFVVLGTLASVLNGTVHPVFSIIIPAKIITMFGNNDKTTLKHDAEIYSMIFVLGVI 746
QY 301 CFVSYFMQGLFYGRAGEILTWLRLHAFKAMLYQDIAMPDEKENSTGGTTLTILADIAOI 360
DB 747 CFVSYFM-----QDIAMPDEKENSTGGTTLTILADIAOI 780
QY 361 QGATSGRIGVLTONATNMGLSVIIISPIYGWEMTFLISLAPVLAVTGMETAAMTGFANK 420
DB 781 QGATSGRIGVLTONATNMGLSVIIISPIYGWEMTFLISLAPVLAVTGMETAAMTGFANK 840
QY 421 DKQELKHAGKIATEALENIRTIIVSLTREKAPROMYEMMLOTHRTSKKAOIIGSCYAFS 480
DB 841 DKQELKHAGKIATEALENIRTIIVSLTREKAPROMYEMMLOTHRTSKKAOIIGSCYAFS 900
QY 481 HAFIYFAYAAAGFRFGAYLIQAGRWTPGEGFIVFTAIYAGAMAIGETLVLAPEYSKAKSGA 540
DB 901 HAFIYFAYAAAGFRFGAYLIQAGRWTPGEGFIVFTAIYAGAMAIGETLVLAPEYSKAKSGA 960
QY 541 AHLFALLEKKPNIDRSQSGKKPDTCEGNLEPREVSFFPCPDVFIILRGLSLSTERGKT 600
DB 961 AHLFALLEKKPNIDRSQSGKKPDTCEGNLEPREVSFFPCPDVFIILRGLSLSTERGKT 1020
QY 601 VAFVSGSGGKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQWLSQIAIIVPQEPVLENC 660
DB 1021 VAFVSGSGGKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQWLSQIAIIVPQEPVLENC 1080
QY 661 STAENIAYGDNRSRVVPLDBIKEAANAANTHSFIEGLPEKINTQVGLKGHQLSGGQKORLA 720
DB 1081 STAENIAYGDNRSRVVPLDBIKEAANAANTHSFIEGLPEKINTQVGLKGHQLSGGQKORLA 1140
QY 721 IARALLQKPKILLDEATSALDNSEKVVQHALDKARTGRTCLVWTHRLSAIQNADLIIV 780
DB 1141 IARALLQKPKILLDEATSALDNSEKVVQHALDKARTGRTCLVWTHRLSAIQNADLIIV 1200
QY 781 LHNGKIKEQSTHQLLRNRDIYFKLVNAQSVQ 812
DB 1201 LHNGKIKEQSTHQLLRNRDIYFKLVNAQSVQ 1232

RESULT 6

US-09-873-409-1
; Sequence 1, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-409-1

Query Match 81.5%; Score 3323; DB 9; Length 659;
Best Local Similarity 100.0%; Pred. No. 1,2e-290; Indels 0; Gaps 0;
Matches 659; Conservative 0; Mismatches 0;

QY 154 MLAEGAHAELMAKRGLYSLVMSQDIKKADEQMSMTYSTERTKNSPLHSVKSISKDF 213
DB 1 MLAEGAHAELMAKRGLYSLVMSQDIKKADEQMSMTYSTERTKNSPLHSVKSISKDF 60
QY 214 IDKABESTOSKEISLPEVSLKILKLNKPEVPVLTGLASVLNGTVHPVFSIIIPAKIIT 273
DB 61 IDKABESTOSKEISLPEVSLKILKLNKPEVPVLTGLASVLNGTVHPVFSIIIPAKIIT 120
QY 274 MFGNNDKTTLKHDAEIYSMIFVLGVIKVFYVMOGLFYGRAGEILTWLRLHAFKAMLY 333

Db 121 MFGNDKTTLKHDAEYISMIFVLGVICFVSFYMQGLFYGRAGEIILTRLRLHAPKAMLY 180
QY 334 QDIAMDEKENSNGGLTTLAIDIAIOQATGSRIGVLTONATNMGSLVSIISFYGEMT 393
Db 181 QDIAMDEKENSNGGLTTLAIDIAIOQATGSRIGVLTONATNMGSLVSIISFYGEMT 240
QY 394 FLILSIAPVLAVTGMETAMTGFANKDKQELKHAGKIAATEALENIRTIIVSLTRKAPBQ 453
Db 241 FLILSIAPVLAVTGMETAMTGFANKDKQELKHAGKIAATEALENIRTIIVSLTRKAPBQ 300
QY 454 MYEMELQTHRNSTKKAQIIGSCVAFSHAFIYFAYAGFRFGAYLQAGRWTPGEMFIYF 513
Db 301 MYEMELQTHRNSTKKAQIIGSCVAFSHAFIYFAYAGFRFGAYLQAGRWTPGEMFIYF 360
QY 514 TAIYAGAMAIGKTLVLAPESKAKSAGAAHLFALLEKXPNIDRSQBGKXPDTCGNLEPR 573
Db 361 TAIYAGAMAIGKTLVLAPESKAKSAGAAHLFALLEKXPNIDRSQBGKXPDTCGNLEPR 420
QY 574 EVSFFPCRPDVTILRGLSLSIRGKTVAFVGGSGCKSTSVQLLQRLYDPVQGVLFQD 633
Db 421 EVSFFPCRPDVTILRGLSLSIRGKTVAFVGGSGCKSTSVQLLQRLYDPVQGVLFQD 480
QY 634 VDAKELNVQLRSQIAIVPQEPVLFNGCSIAENIAYGDNRSRVVPLDRIKAAANAHTSP 693
Db 481 VDAKELNVQLRSQIAIVPQEPVLFNGCSIAENIAYGDNRSRVVPLDRIKAAANAHTSP 540
QY 694 EGLPEKNTQVGLKGAQLSGGQKQRIAIARALLOKPKILLDEATGALDNDSEKVVQHAL 753
Db 541 EGLPEKNTQVGLKGAQLSGGQKQRIAIARALLOKPKILLDEATGALDNDSEKVVQHAL 600
QY 754 DKARTGRTCLVTHRLSAIONADLIIVLHNGKIKEQGTTHOELLNRNDIYFKLVNAQSVQ 812
Db 601 DKARTGRTCLVTHRLSAIONADLIIVLHNGKIKEQGTTHOELLNRNDIYFKLVNAQSVQ 659

RESULT 7
US-10-092-900A-304
; Sequence 304, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Bsha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C

; CURRENT APPLICATION NUMBER: US/10/092,900A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 304
; LENGTH: 1354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-900A-304

Query Match 77.7%; Score 3168.5; DB 12; Length 1354;
Best Local Similarity 76.8%; Pred. No. 3.6e-276;
Matches 677; Conservative 30; Mismatches 62; Indels 113; Gaps 14;

QY 2 VDENDIRALNVHRDHIGVNSQEPVLFGTTTISNKKIGRDD--VTDEKKEAAREANAY 59
Db 455 VDGVDKELNVQLRSQIAIVPQEPVLFNGCSIAENIAYGDNRSRVVPLDRIKAAANAHT 514
QY 60 DEIMFPNKPNTLVGSKGAGMSGGQKQRIAIARALVRNPKIILDEATGALDNDSEK 118
Db 515 SFIEGLPEKNTQVGLKGAQLSGGQKQRIAIARALLOKPKILLDEATGALDNDSE 574
QY 119 QAALEK----- 124
Db 575 QHALDKARTGRTCLVTHRLSAIONADLIIVLHNGKIKEQGTTHOELLNRNDIYFKLVNAQ 634
QY 125 -ASKGRTTIWAHRLSTIRSDLIIVTLKDGMLAEKGAHAEKGLVYSLVMSQDIKKA 183
Db 635 SASKGRTTIWAHRLSTIRSDLIIVTLKDGMLAEKGAHAEKGLVYSLVMSQ----- 689
QY 184 DEQMESMTYSTRKTNLSPLHSVKSISGDFIDKABESTQSKEISLPEVSLKILKLNKPE 243
Db 690 -----VLMGTLSDCGN-----SLPEVSLKILKLNKPE 718
QY 244 NPPVVLGTLASVLNGTVHVPFSIIIAKIIIT-MFGNNDKTTLKHDAEIIYSMIFVLGV--- 299
Db 719 NPPVVLGTLASVLNGTVHVPFSIIIAKIIITVMPGNND---LFFFLKIFLYSLFLPKOG 775
QY 300 --ICPVSVFMQGLFYGRAGEIILTMLRLHAFKAMLYQDIAWFEDEKENSTGGLTTLAIDI 357
Db 776 PSVDPCLPFAQGLFYGRAGEIILTMLRLHAFKAMLYQDIAWFEDEKENSTGGLTTLAIDI 835
QY 358 AOIQGATGSRIGVLTONATNMGSLVSIISFYGEMTFLILSIAPVLAVTGMETAMTGF 417
Db 836 AOIQGATGSRIGVLTONATNMGSLVSIISFYGEMTFLILSIAPVLAVTGMETAMTGF 895
QY 418 ANKDKQELKHAG--KIATEALENIRTIIVSLTRKAPBQMYEEMLOTOH-RNTSKKAQIIG 474
Db 896 ANKDKQELKHAGKVIATEALENIRTIIVSLTRKAPBQMYEEMLOTOHRRNTSKKAQIIG 955
QY 475 SCYAFSHAFIYFAYAGFRFGAYLQAGRWTPGEMFIYFTAIYAGAMAIGKTLVLAP 533
Db 956 SCYAFSHAFIYFAYAGFRFGAYLQAGRWTPGEMFIYFTAIYAGAMAIGKTLVLAP 1015

QY 534 SKAKGAHLFALLEKKXPNIDSRSOEGKDP---DTCENLLEFREVFFYPYCRDPVILRG 590
DB 1016 SKAKGAHLFALLEKKXPNIDSRSOEGKDP---DTCENLLEFREVFFYPYCRDPVILRG 1075
QY 591 LSLSIEGKTVAFVSSGCKSTSVQLLORLYDPVQGVLFDPGVDAKELNVQWLSQIAI 650
DB 1076 LSLSIEGKTVAFVSSGCKSTSVQLLORLYDPVQGVLFDPGVDAKELNVQWLSQIAI 1135
QY 651 VPOEVLFNCSIAENIAYGNSRVVPLDEIKKANAANIHSHFIEGLPEKYNTOVGLKGAQ 710
DB 1136 VPOEVLFNCSIAENIAYGNSRVVPLDEIKKANAANIHSHFIEGLPEKYNTOVGLKGAQ 1194
QY 711 LSGGOKORLAIALALLOKPKILLDEATSAIDNDSEK--VVOHALDKARTGRTCLVWVTH 768
DB 1195 LSGGOKORLAIALALLOKPKILLDEATSAIDNDSEK--VVOHALDKARTGRTCLVWVTH 1254
QY 769 LSAIQNADLIIVLHNGKIKQOQTHOELLNRNDIYFKLVNAQS 810
DB 1255 LSAIQNADLIIVLHNGKIKQOQTHOELLNRNDIYFKLVNAQS 1296

RESULT 8
US-09-817-762-5
; Sequence 5, Application US/09817762
; Publication No. US20020068344A1
; GENERAL INFORMATION:
; APPLICANT: Spalding, Edgar P.
; APPLICANT: Non, Bosi
; TITLE OF INVENTION: MDR-like ABC Transporter Gene From
; FILE REFERENCE: 13238-00061
; CURRENT APPLICATION NUMBER: US/09/817,762
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: PCT/US99/22363
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: US 60/101,814
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1066
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank P21439
; DATABASE ENTRY DATE: 1998-07-15
US-09-817-762-5

Query Match 60.4%; Score 2465.5; DB 12; Length 1066;
Best Local Similarity 58.3%; Pred. No. 7.3e-213;
Matches 478; Conservative 149; Mismatches 182; Indels 11; Gaps 3;
QY 2 VDNDRALNVHRHGHVSVQEPVLPFTTISNNIKYGRDVTDEEMERAAEANYDF 61
DB 242 IDGQDIRNFNVNLYREIIGVSVQEPVLPFTTIAENICYGRGNVTWDEIKKAVKEANAYEF 301
QY 62 IMEPNFKNTLVGKGAQMSGGOKORLAIALALVNPKNILDEATSAIDSEKSAVQAA 121
DB 302 IMKLPOKFDTLVGRGAQSGGOKORLAIALALVNPKNILDEATSAIDSEKSAVQAA 361
QY 122 LKASKGRITTVIARLSITRADIIVTLKGMALAKGAHAEIMAKRGVYSLV----- 175
DB 362 LKASKGRITTVIARLSITRADIIVTLKGMALAKGAHAEIMAKRGVYSLV----- 421
QY 176 ---MSQDIKABQEMESWYTERKTNLSPLHSVKSIIK-SDFIDKA-BESTQSKEISLPE 230
DB 422 SQTQSEFEFLNDEKATRAMPNKWSRLFRHSTQKNLNSQCSQSLDVTGDLGANVPP 481
QY 231 VSLIKTLKLNKBPWPVVLGTLASVLNGTVHPVPSIIPAKIITMFGNNDKTKLKHDAIY 290
DB 482 VSLFKVLKLNKWPVFPVGTVCATANGGLQPAFSPVIFSEIIAIFPGDGDVAKQCKNIP 541

QY 291 SMIFVLGVICFVSFMOGLFYGRAGEILTWELRHAFKAMLYQDIAMFDEKENSTGGIT 350
DB 542 SMIFVLGVICFVSFMOGLFYGRAGEILTWELRHAFKAMLYQDIAMFDEKENSTGGIT 601
QY 351 TILALIDIAIQCATSRICVLITQATNNMGLSVIISFIYGWMTFLILSIAPVLAVTGMIE 410
DB 602 TRLATDAQVQCATGTRLALIAQNIANLGTIIISFIYGWMTFLILSIAPVLAVTGMIE 661
QY 411 TAAMTGPANKQOELKHAGKINTEALENIRTVISLREKAPQCYEEMLQTOHRNTSKA 470
DB 662 MGLLAGNAKRDCKKELEAGKIAEAIENIRTVISLREKAPQCYEEMLQTOHRNTSKA 721
QY 471 QIIGSCYAPSHAFIYFAVAAGFRFGAYLITQAGRTPEGMPIVFTAIYAGAMAIGKTLVA 530
DB 722 HIYGITPISQAFMYFSYAGCFRFGAYLIVNGHMRFRDVLVFSALVFGAVALGHASSPA 781
QY 531 PRYSKAKSAAHLFALLEKKXPNIDSRSOEGKDPDTCENLLEFREVFFYPYCRDPVILRG 590
DB 782 PDYAKAKLSAHLFMLEFQPLIDSYSEBGLKDPFBGNITTFNEVVFNTPTTANPVLAG 841
QY 591 LSLSIEGKTVAFVSSGCKSTSVQLLORLYDPVQGVLFDPGVDAKELNVQWLSQIAI 650
DB 842 LSLVKKGGTALVSSGCKSTVOLLERFYDPLAGTVLLDQGEAKLNVQWLSQIAI 901
QY 651 VPOEVLFNCSIAENIAYGNSRVVPLDEIKKANAANIHSHFIEGLPEKYNTOVGLKGAQ 710
DB 902 VSOEPLFDCSIAENIAYGNSRVVSDIEIVSAAKAAANHPFIETLPHKYETRVGDKGTQ 961
QY 711 LSGGOKORLAIALALLOKPKILLDEATSAIDNDSEKVVQHALDKARTGRTCLVWVTH 770
DB 962 LSGGOKORLAIALALLOKPKILLDEATSAIDNDSEKVVQHALDKARTGRTCLVWVTH 1021
QY 771 AIONADLIIVLHNGKIKQOQTHOELLNRNDIYFKLVNAQS 810
DB 1022 TIQNAADLIIVFQNGRVKRGHGTQQLLAQKGIYFPMVSVQAA 1061

RESULT 9
US-10-363-112-49
; Sequence 49, Application US/10363112
; Publication No. US20040091964A1
; GENERAL INFORMATION:
; APPLICANT: THE AUSTRALIAN NATIONAL UNIVERSITY
; APPLICANT: BOARD, PHILLIP
; APPLICANT: HARRIS, MATTHEW
; TITLE OF INVENTION: MODIFIED PROTEINS, ISOLATED NOVEL PEPTIDES, AND USES THEREOF
; FILE REFERENCE: 007643-0302189
; CURRENT APPLICATION NUMBER: US/10/363,112
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/AU01/01093
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,663
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 1275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-112-49

Query Match 60.4%; Score 2465.5; DB 16; Length 1275;
Best Local Similarity 58.3%; Pred. No. 9.9e-213;
Matches 478; Conservative 149; Mismatches 182; Indels 11; Gaps 3;
QY 2 VDNDRALNVHRHGHVSVQEPVLPFTTISNNIKYGRDVTDEEMERAAEANYDF 61
DB 455 IDGQDIRNFNVNLYREIIGVSVQEPVLPFTTIAENICYGRGNVTWDEIKKAVKEANAYEF 514
QY 62 IMEPNFKNTLVGKGAQMSGGOKORLAIALALVNPKNILDEATSAIDSEKSAVQAA 121
DB 515 IMKLPOKFDTLVGRGAQSGGOKORLAIALALVNPKNILDEATSAIDSEKSAVQAA 574


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; SEQ ID NO 8
; LENGTH: 1281
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-10-101-433A-8

Query Match      59.9%; Score 2442; DB 14; Length 1281;
Best Local Similarity 56.8%; Pred. No. 1.3e-210;
Matches 469; Conservative 160; Mismatches 178; Indels 18; Gaps 4;

QY 2 VDENDIRALNVRYDDHIGVVSQEPVLFGTTISNNIKYGRDDVTDDEMERAAEANAAYDF 61
DB 455 IDGQDIRTINVRLREITGVVSQEPVLFGTTISNNIKYGRDDVTDDEMERAAEANAAYDF 514
QY 62 IMEPNKNFTLVGEGKGAOMSGGQKORIAIARALVRNPKILILDEATSALDSKSAVQAA 121
DB 515 IMKLPNKFPTLVGERGAQLSGGQKORIAIARALVRNPKILILDEATSALDSKSAVQAA 574
QY 122 LEKASKGRTTIVVAHRLSTIRADLIIVTLKGMLEAKGAHAELMAKRGILYSLVMSQDIK 181
DB 575 LDKARKGRTTIVIAHRLSTVRNADVIAGFDGVIIVEXGNHDELMKEKGIYFKLVMTQ-TR 633
QY 182 KADQESMTYSTERTKNSLPLHSVKSIKSDFI-----DKAESSTOSKEI 226
DB 634 GNEIELENATGESKESDALEM-SPKDSGSLIKRSTRSIIHAPQGDRLGTEDLNE 692
QY 227 SLPEVSLKILKLNKPEWPFVVLGTASVLNCTVHPVFSIIFAKIITMF-GNNDKTTLKH 285
DB 693 NVPPVSFWRLKLNSTWEPYFVVGIFCAIINGGLQPAFSIIFSRIGIFTRDEDPETKQ 752
QY 286 DAEIVSMIFVLGVICVSVFMQGLFYGRAGILTMRLHLAKMAYQDIAMFDEKENS 345
DB 753 NSNMFSLVLVIGIISITIFLQGTFFKAGELITKRLRYMFRSMURQDVSWFDDPKNT 812
QY 346 TGGTTLTILADIAIQGATSGRIGVLTONATNMGLSVIISFIYGMETFLIISIAPVLAV 405
DB 813 TGAUTRLANDAQAQVKAIGSRLAVITONIANLGTGIIISLIYGMQLTLLLAIVPIAI 872
QY 406 TGMETAAITGANKDKQELKAGKIATEALENIITVSLTREKAPQOMYEMLOTHRN 465
DB 873 AGVVEKMLSGQALKDKKELEGAGKIATEALENITVSLTREKAPQOMYEMLOTHRN 932
QY 466 TSKKAQIIGSCYAFSHAFIYFAYAGFRFGAYLIQAGRMTPEGMFIVFTAIAYGAMAIGK 525
DB 933 SLRKAHIFGVFSITQAMMYFSYAGCFRFGAYLVANEFMNFQDVLVPSAIVFGAMAVGQ 992
QY 526 TLVLAPYSKAKSAAHLFALLEKPNIDRSQEGKPKDTCGNLEPREVSFFPCRPDV 585
DB 993 VSSFAPDYAKAVGAAHVIMIIEKSPIDISYSPHGLKNTLEGNTFENVVFNPTRPDI 1052
QY 586 FILRGLSLIERGKTAVFVSGSGCGKSTSVOLLQRLYDPOGVLPDGVDAKELNVQWLR 645
DB 1053 PVLQGLSEVKGQTALVSGSGCGKSTVVQLLERFYDPLAGSVLIDGKEIKHLNVQWLR 1112
QY 646 SQIAIVPQEPVLFNCSIAENIAYGNSRWVPLDEIKEAANAANIHSFIEGLPEKYNTOVG 705
DB 1113 AHLGIVSQEPILFDCSIAENIAYGNSRWVSHEEIMQAANEANIHHFIETLPEKYNTRVG 1172
QY 706 LKGAQLSGGQKORIAIARALVRNPKILILDEATSALDSKSAVQAA 765
DB 1173 DKGTLQSGGQKORIAIARALVRNPKILILDEATSALDSKSAVQAA 1232
QY 766 THRLSAIGNADLIIVLHNGKIKEQTHQELLNRDIYFKLVNAQS 810
DB 1233 AHRLLSTIQNADLIIVFQNGKVKERHGTQOILLAQRGIVFSKVSQA 1277

RESULT 12
US-10-101-433A-9
; Sequence 9, Application US/10101433A
; Publication No. US20030119726A1
; GENERAL INFORMATION:
; APPLICANT: Hanscom, Sara

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; APPLICANT: Crespi, Charles
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G00307/70019
; CURRENT APPLICATION NUMBER: US/10/101,433A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/277,095
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 1281
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-10-101-433A-9

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Query Match      59.9%; Score 2442; DB 14; Length 1281;
Best Local Similarity 56.8%; Pred. No. 1.3e-210;
Matches 469; Conservative 160; Mismatches 178; Indels 18; Gaps 4;

QY 2 VDENDIRALNVRYDDHIGVVSQEPVLFGTTISNNIKYGRDDVTDDEMERAAEANAAYDF 61
DB 455 IDGQDIRTINVRLREITGVVSQEPVLFGTTISNNIKYGRDDVTDDEMERAAEANAAYDF 514
QY 62 IMEPNKNFTLVGEGKGAOMSGGQKORIAIARALVRNPKILILDEATSALDSKSAVQAA 121
DB 515 IMKLPNKFPTLVGERGAQLSGGQKORIAIARALVRNPKILILDEATSALDSKSAVQAA 574
QY 122 LEKASKGRTTIVVAHRLSTIRADLIIVTLKGMLEAKGAHAELMAKRGILYSLVMSQDIK 181
DB 575 LDKARKGRTTIVIAHRLSTVRNADVIAGFDGVIIVEXGNHDELMKEKGIYFKLVMTQ-TR 633
QY 182 KADQESMTYSTERTKNSLPLHSVKSIKSDFI-----DKAESSTOSKEI 226
DB 634 GNEIELENATGESKESDALEM-SPKDSGSLIKRSTRSIIHAPQGDRLGTEDLNE 692
QY 227 SLPEVSLKILKLNKPEWPFVVLGTASVLNCTVHPVFSIIFAKIITMF-GNNDKTTLKH 285
DB 693 NVPPVSFWRLKLNSTWEPYFVVGIFCAIINGGLQPAFSIIFSRIGIFTRDEDPETKQ 752
QY 286 DAEIVSMIFVLGVICVSVFMQGLFYGRAGILTMRLHLAKMAYQDIAMFDEKENS 345
DB 753 NSNMFSLVLVIGIISITIFLQGTFFKAGELITKRLRYMFRSMURQDVSWFDDPKNT 812
QY 346 TGGTTLTILADIAIQGATSGRIGVLTONATNMGLSVIISFIYGMETFLIISIAPVLAV 405
DB 813 TGAUTRLANDAQAQVKAIGSRLAVITONIANLGTGIIISLIYGMQLTLLLAIVPIAI 872
QY 406 TGMETAAITGANKDKQELKAGKIATEALENIITVSLTREKAPQOMYEMLOTHRN 465
DB 873 AGVVEKMLSGQALKDKKELEGAGKIATEALENITVSLTREKAPQOMYEMLOTHRN 932
QY 466 TSKKAQIIGSCYAFSHAFIYFAYAGFRFGAYLIQAGRMTPEGMFIVFTAIAYGAMAIGK 525
DB 933 SLRKAHIFGVFSITQAMMYFSYAGCFRFGAYLVANEFMNFQDVLVPSAIVFGAMAVGQ 992
QY 526 TLVLAPYSKAKSAAHLFALLEKPNIDRSQEGKPKDTCGNLEPREVSFFPCRPDV 585
DB 993 VSSFAPDYAKAVGAAHVIMIIEKSPIDISYSPHGLKNTLEGNTFENVVFNPTRPDI 1052
QY 586 FILRGLSLIERGKTAVFVSGSGCGKSTSVOLLQRLYDPOGVLPDGVDAKELNVQWLR 645
DB 1053 PVLQGLSEVKGQTALVSGSGCGKSTVVQLLERFYDPLAGSVLIDGKEIKHLNVQWLR 1112
QY 646 SQIAIVPQEPVLFNCSIAENIAYGNSRWVPLDEIKEAANAANIHSFIEGLPEKYNTOVG 705
DB 1113 AHLGIVSQEPILFDCSIAENIAYGNSRWVSHEEIMQAANEANIHHFIETLPEKYNTRVG 1172
QY 706 LKGAQLSGGQKORIAIARALVRNPKILILDEATSALDSKSAVQAA 765
DB 1173 DKGTLQSGGQKORIAIARALVRNPKILILDEATSALDSKSAVQAA 1232
QY 766 THRLSAIGNADLIIVLHNGKIKEQTHQELLNRDIYFKLVNAQS 810
DB 1233 AHRLLSTIQNADLIIVFQNGKVKERHGTQOILLAQRGIVFSKVSQA 1277

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Db 1233 ARLSTIQNADLIWVFGKVKKEGTHQQLAOKGIYFSMVQQA 1277

RESULT 13

US-09-769-097-2

Sequence 2, Application US/09769097

Patent No. US20020055128A1

GENERAL INFORMATION:

APPLICANT: Kimberly Anne Brun

APPLICANT: Richard James Chenery

APPLICANT: Harma Ellens

APPLICANT: John Anthony Feild

APPLICANT: Lin Yue

TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES

FILE REFERENCE: GP-50009-C2

CURRENT APPLICATION NUMBER: US/09/769,097

PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 09/208,809

PRIOR FILING DATE: 1998-12-09

PRIOR APPLICATION NUMBER: 09/156,800

PRIOR FILING DATE: 1999-09-17

PRIOR APPLICATION NUMBER: US99/20770

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 1272

TYPE: PRT

ORGANISM: RATTUS RATTUS

US-09-769-097-2

Query Match 59.8%; Score 2441; DB 9; Length 1272;

Best Local Similarity 57.1%; Pred. No. 1.6e-210;

Matches 470; Conservative 164; Mismatches 175; Indels 14; Gaps 5;

Qy 2 VDENDIRALNVRHYRDHIGVVSQEPVLTGTTISNNIKYGRDDVTDSEMERAREANAYDF 61

Db 445 IDGQDRTINVRYLEIIGVVSQEPVLTATTIAENIRYGRNVTDSEMERAREANAYDF 504

Qy 62 IMEFNKNFTLVGKGAQSGGKQRIARALVRNPKILILDEATSDSEKSAVQAA 121

Db 505 IMKLPHKEDTLVGERGAQLSGGKQRIARALVRNPKILILDEATSDSEKSAVQAA 564

Qy 122 LEKASGRTTIVVAHRLSTIRADIVTLKDGMLAEKGAHAEIMAKRGLIYSLVMSQ--- 178

Db 565 LDKAREGRTTIVIAHRLSTVRNADYVAGFDGGVIVGQGNHDELMREKGIYFLVMTQTAG 624

Qy 179 -DIKKADEQMES-----MTYSTERKTNLS--PLHSVKSISKDFIDKABEST--OSKEISL 228

Db 625 NEIELGNACESKDGIDNVDMSSKDSGLIRRRSTRKIRGPHDQDGLSTKEALDDV 684

Qy 229 PEVSLKILKLNKPEWPFVLTGLASVINGTVHPVFSIIFAKIIITWFGNNDKTL-KHDA 287

Db 685 PPASFWRILKLNSTWPFVGVFCAIINGGLQPAFSAIIFSKVGVFTKNDTPETQONS 744

Db 1233 ARLSTIQNADLIWVFGKVKKEGTHQQLAOKGIYFSMVQQA 1277

RESULT 13

US-09-769-097-2

Sequence 2, Application US/09769097

Patent No. US20020055128A1

GENERAL INFORMATION:

APPLICANT: Kimberly Anne Brun

APPLICANT: Richard James Chenery

APPLICANT: Harma Ellens

APPLICANT: John Anthony Feild

APPLICANT: Lin Yue

TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES

FILE REFERENCE: GP-50009-C2

CURRENT APPLICATION NUMBER: US/09/769,097

PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 09/208,809

PRIOR FILING DATE: 1998-12-09

PRIOR APPLICATION NUMBER: 09/156,800

PRIOR FILING DATE: 1999-09-17

PRIOR APPLICATION NUMBER: US99/20770

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 1272

TYPE: PRT

ORGANISM: RATTUS RATTUS

US-09-769-097-2

Query Match 59.8%; Score 2441; DB 9; Length 1272;

Best Local Similarity 57.1%; Pred. No. 1.6e-210;

Matches 470; Conservative 164; Mismatches 175; Indels 14; Gaps 5;

Qy 2 VDENDIRALNVRHYRDHIGVVSQEPVLTGTTISNNIKYGRDDVTDSEMERAREANAYDF 61

Db 445 IDGQDRTINVRYLEIIGVVSQEPVLTATTIAENIRYGRNVTDSEMERAREANAYDF 504

Qy 62 IMEFNKNFTLVGKGAQSGGKQRIARALVRNPKILILDEATSDSEKSAVQAA 121

Db 505 IMKLPHKEDTLVGERGAQLSGGKQRIARALVRNPKILILDEATSDSEKSAVQAA 564

Qy 122 LEKASGRTTIVVAHRLSTIRADIVTLKDGMLAEKGAHAEIMAKRGLIYSLVMSQ--- 178

Db 565 LDKAREGRTTIVIAHRLSTVRNADYVAGFDGGVIVGQGNHDELMREKGIYFLVMTQTAG 624

Qy 179 -DIKKADEQMES-----MTYSTERKTNLS--PLHSVKSISKDFIDKABEST--OSKEISL 228

Db 625 NEIELGNACESKDGIDNVDMSSKDSGLIRRRSTRKIRGPHDQDGLSTKEALDDV 684

Qy 229 PEVSLKILKLNKPEWPFVLTGLASVINGTVHPVFSIIFAKIIITWFGNNDKTL-KHDA 287

Db 685 PPASFWRILKLNSTWPFVGVFCAIINGGLQPAFSAIIFSKVGVFTKNDTPETQONS 744

Qy 288 EIVSMIFVILGVCVSYFPMQGLFYGRAGSILTMRLHLAFKAMLYQDIAMFDEKENSTG 347

Db 745 NLFSLFLIIGIISFTTFLQGTFTFGKAGSILTKRLRYMFKSMRLQDISWFDPKNTTG 804

Qy 348 GLTILAIIDAQTCAGTSIGVLTQWATMGLSVIISPIYGHMTFFLISIAPLAVTG 407

Db 805 ALTRLANDAAQVKATGTSRLAVITQNIAMGLGIIISLYGQLTLLAIYPIIATAG 864

Qy 408 MISTAMTGFANDKQELKHAGKIAETALENIRITIVSLTREKAFQWYEMLOTOHNTS 467

Db 865 VVEMWLSGQALKKKELESGKIAETAIENFTVVSILTREKAFQWYAGSLQIPIYNAL 924

Qy 468 KKAQIGSCVAFSHAFTYFAYAGFRPAGVLIQAGRTWPEGMTFVITAYAGMAIKGTL 527

Db 925 KKAHVFGITTSFTQAMMYFSYAACFRDAYLVARELMTFENVLLVFSALVFGAMVQVS 984

Qy 528 VLAPEYSKAKSAAHLLFALLEKKPNIDSRSECKKPDTCBGNLEPREVSFFYPCRPDVI 587

QY 288 EIYSMIFVLGVICFVSFMOGLFYGRAGEILTVRLHRLAFKAMLYODIAWFDEKENSTG 347
 DB 745 NLFSLFLVLIIIFITFLFQGFYGRAGEILTVRLHRLAFKAMLYODIAWFDEKENSTG 804
 QY 348 GLTTLAIDIAIQCATGSRIGVLTQATNMGSLVSIIFSYGEMTFLIISIAPLAVTG 407
 DB 805 ALTLRLANDAQQVKGATSLAVITQNTANLGTGIIISLIYGMQLTLLLAIVPIIAIAG 864
 QY 408 MIETAMTGFANKQKQELKHAGKIATEALENIRIVSLTRKAFQEMVEMLOTHRNTS 467
 DB 865 VVEMKMLSGQALDKKXLEGSGKIATEALENIRIVSLTRKAFQEMVEMLOTHRNTS 924
 QY 468 KKAQIIGSCYAFSHAFIYFAAAGFRFGAYLIQAGRTPEGMFTVFTAIAYGAMAIGKTL 527
 DB 925 KKAHVGITFTFTQAMWYFSAACFRFDAYLVARELMTFENVLVFSAIVFGANAVQVS 984
 QY 528 VLAPYSKAKSGAAHLFALLKKNIDRSQEGKKPDTCEGNLEFREVSFPYPCRPDVI 587
 DB 985 SFAPQYAKAVSASHIIRIEIKPEIDSYSTEGKPNMKNLEGNKFNKFNKFNKFNK 1044
 QY 588 LRGSLSTERGKTVAFCVSSGCGKSTSVQLLQRLYDVPQGVLDGVDKELNVMQLRSQ 647
 DB 1045 LQGLSLEVKQOTLALVSSGCGKSTVQLLERFYDPMAGTVFLDGKEIKQLNVMQLRAH 1104
 QY 648 IAIYQEPVLPNCISIAENIAYGDSNRVVPVLDDEIKEAANAANIHSFIEGLPEKYNQVGLK 707
 DB 1105 LGIVSQEPILFDCSLAENIAYGDSNRVVPVSHKEIVKAAKEANIHOPIDSLPEKYNTRVGDK 1164
 QY 708 GAQISGGQKORLAIARALLQKPKILLDEATSLDNDSEKVVQHALDKARTGRTCLVTH 767
 DB 1165 GQLSGGQKQRIARALVRPHILLDEATSLDNDSEKVVQHALDKARTGRTCLVTH 1224
 QY 768 RLSTAIQADLIIVLHNGKIKQGTQBELLRNDRYFKLVNAQS 810
 DB 1225 RLSTAIQADLIIVLHNGKIKQGTQBELLRNDRYFKLVNAQS 1267
 RESULT 15
 US-10-101-433A-3
 ; Sequence 3, Application US/10101433A
 ; Publication No. US20030119726A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hanscom, Sara
 ; APPLICANT: Crespi, Charles
 ; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
 ; FILE REFERENCE: G00307/70019
 ; CURRENT APPLICATION NUMBER: US/10101433A
 ; CURRENT FILING DATE: 2002-03-19
 ; PRIOR APPLICATION NUMBER: US 60/277,095
 ; PRIOR FILING DATE: 2001-03-19
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 1280
 ; TYPE: PRT
 ; ORGANISM: Macaca fascicularis
 US-10-101-433A-3

Query Match 59.8%; Score 2441; DB 14; Length 1280;
 Best Local Similarity 56.4%; Pred. No. 1.6e-210;
 Matches 465; Conservative 168; Mismatches 174; Indels 18; Gaps 5;
 QY 2 VDENDIRALNVRHDIHGVSWQEPVLPFGTITSNKIKYGRDDVDTEEMERARBANAYDF 61
 DB 453 VQGDRIINVAFLREIIGVSWQEPVLPFGTITSNKIKYGRDDVDTEEMERARBANAYDF 512
 QY 62 IMEPFNKNTLVGKGAQNSGQKQRIARALVRNPKILLDEATSLDSEKSAVQAA 121
 DB 513 INKLPQKFTLVGKGAQNSGQKQRIARALVRNPKILLDEATSLDSEKSAVQAA 572
 QY 122 LEKASKGRTIIVAHRLSTIRADLIIVLHNGKIKQGTQBELLRNDRYFKLVNAQS 180
 DB 573 LDKARKGRTIIVAHRLSTIRADLIIVLHNGKIKQGTQBELLRNDRYFKLVNAQS 632

QY 181 -----KKADE---QMESMTYSTERKTNLSL-----PLHSVKSITKSDPIDKABESTOSKEI 236
 DB 633 NEIELENAADESKSEIDITLLESSHDSGLIRKSTRSRVRSQGO--DRKLSSTKALDE 690
 QY 227 SLPEVSLKILKLNKPEWPFVVLGTILASVLNGTVHPVFSIIIFAKIITMF-GNNDKTTLKH 285
 DB 691 SIPPVSFMRIMKLNLTWEPYVGVPCALINGLOPAPAFVFSKIIGIETFRNDDAETKRQ 750
 QY 286 DAEIYSMIFVLGVICFVSFMOGLFYGRAGEILTVRLHRLAFKAMLYODIAWFDEKENSTG 345
 DB 751 NSLFLSLLFLVLGVIFITFTFQGFYGRAGEILTVRLHRLAFKAMLYODIAWFDEKENSTG 810
 QY 346 TGLTTLAIDIAIQCATGSRIGVLTQATNMGSLVSIIFSYGEMTFLIISIAPLAV 405
 DB 811 TGLTTLRLANDAQQVKGATSLAVITQNTANLGTGIIISLIYGMQLTLLLAIVPIIAI 870
 QY 406 TGMETAMTGFANKQKQELKHAGKIATEALENIRIVSLTRKAFQEMVEMLOTHRNTS 465
 DB 871 AGVEMKMLSGQALDKKXLEGSGKIATEALENIRIVSLTRKAFQEMVEMLOTHRNTS 930
 QY 466 TSKAQIIGSCYAFSHAFIYFAAAGFRFGAYLIQAGRTPEGMFTVFTAIAYGAMAIGK 525
 DB 931 SLRKAHIFGITFTFTQAMWYFSAACFRFDAYLVARELMTFENVLVFSAIVFGANAVQ 990
 QY 526 TLVLAPYSKAKSGAAHLFALLKKNIDRSQEGKKPDTCEGNLEFREVSFPYPCRPDVI 585
 DB 991 VSSFAPDYAKAVSASHIIRIEIKPEIDSYSTEGKPNMKNLEGNKFNKFNKFNKFNK 1050
 QY 586 FILRGLSLSTERGKTVAFCVSSGCGKSTSVQLLQRLYDVPQGVLDGVDKELNVMQLR 645
 DB 1051 PVLQGLSLEVKQOTLALVSSGCGKSTVQLLERFYDPMAGTVFLDGKEIKQLNVMQLR 1110
 QY 646 SQIAIYQEPVLPNCISIAENIAYGDSNRVVPVLDDEIKEAANAANIHSFIEGLPEKYNQV 705
 DB 1111 AHLGISVQEPILFDCSLAENIAYGDSNRVVPVSHKEIVKAAKEANIHOPIDSLPEKYN 1170
 QY 706 LKGAQISGGQKORLAIARALLQKPKILLDEATSLDNDSEKVVQHALDKARTGRTCLV 765
 DB 1171 DRGTQLSGGQKQRIARALVRPHILLDEATSLDNDSEKVVQHALDKARTGRTCLV 1230
 QY 766 THRLSAIQADLIIVLHNGKIKQGTQBELLRNDRYFKLVNAQS 810
 DB 1231 AHLSTIQAADLIIVLHNGKIKQGTQBELLRNDRYFKLVNAQS 1275

Search completed: June 24, 2004, 15:24:03
 Job time : 53 secs

Db 751 NSNLSLLFLVLGIVSFITPFLQGFPGKAGEIILTKLRVYVFRSMRLQDVNSFDDPKNT 810
Qy 346 TGGTTLTILADIAIOQAGSRIGVLTONATNMGSLVLIISFYKEMTFILISIAPIAV 405
Db 811 TGLTTRLANDAAQVKGAGSRLAIITQNIANLGVIIISLYGQTLTLLLAIVPIAI 870
Qy 406 TGMTIATMTGAFKNDKQELKAGKIATEALENIRTVSLTRKAFQMYEEMLOTHRN 465
Db 871 AGVYEMXLSQALUKDKLEGAGKIATEALENIRTVSLTRKAFQMYEEMLOTHRN 930
Qy 466 TSKAQIIGSCYAFSAFHAFFAYAGFRFGAYLQAGRWTPGEGFIVFTAIAYGAMAIGK 525
Db 931 SLRKAHIFGITFTQAMMYFSAFHAFFAYAGFRFGAYLQAGRWTPGEGFIVFTAIAYGAMAIGK 990
Qy 526 TLVLAPYSKAKSAAHLPALLEKKNIDSRQSGKGPDTCEGNLBRFVSVFFYPCRPDV 585
Db 991 VSSPAPDYAKAKVSAHHIIMIEKPLDYSYSTGLKPLTEGNVTFNEVVFYPTFLDI 1050
Qy 586 FILGSLISIERGKTVAFFVSGSGGKSTVOLLORLYDPVQGVLDGDAKELNVQWLR 645
Db 1051 PVLGSLSEVKKGTLLALVSGSGGKSTVOLLORLYDPVQGVLDGDAKELNVQWLR 1110
Qy 646 SOIAIVPOBPVLPNCSTAEINAYGNSRWVPLDRIKSAANAANIHSFIEGLPEKINTQVG 705
Db 1111 AHLGIVSQEPILFDCSISEINAYGNSRWVQSEIIVRAAKEANIHFIESLPNKYSTRVG 1170
Qy 706 LKGAQLSGGQKORAIARALVQPHILLDEATSDNDSEKVVQHALDKARTGRTCLV 765
Db 1171 DKGTLQSGGQKORAIARALVQPHILLDEATSDNDSEKVVQHALDKARTGRTCLV 1230
Qy 766 THRLSAIQNADLIVVFNHNGKIKEGQTHOBLNRNDIYFKLVNAQS 810
Db 1231 AHRSTIQNADLIVVFNHNGKIKEGQTHOBLNRNDIYFKLVNAQS 1275

RESULT 2

US-09-672-810-4
; Sequence 4, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEINEL-CRESPI, DOROTHY T.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1283
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-09-672-810-4

Query Match 59.8%; Score 2441; DB 4; Length 1283;
Best Local Similarity 56.4%; Pred. No. 2.7e-229;
Matches 465; Conservative 168; Mismatches 174; Indels 18; Gaps 5;

Qy 2 VDENDIRALNVRHVDHGVTSQSEVPLFGTTISNNIKYGRDVTDEEMERARANAYDF 61
Db 456 VDGQDRTINVRFLREIIGVTSQSEVPLFATTIAENIRYGRDVTDEEMERARANAYDF 515
Qy 62 IMEFPNKENTLVGEGKQWQKORAIARALVNRPKILLDEATSDNDSEKVVQAA 121
Db 516 IMKLPQKEDTLVGERGQALSGGQKORAIARALVNRPKILLDEATSDNDSEKVVQAA 575
Qy 122 LEKASKGRTTIVAHRLSTVRNADVIAGDDGVIVVEKGNHDELMKEKGIYFKLVMTQTAG 180

Db 576 LOKARKGRTTIVAHRLSTVRNADVIAGDDGVIVVEKGNHDELMKEKGIYFKLVMTQTAG 635
Qy 181 -----KKADE---QMESMTYSTERTKNSL-----PLHSVKGIKSDFDIKABESTOSKEI 226
Db 636 NEIETLENADESKSEIDTLEMSHDSGSLIRKSTRSRVSGSQG--DRKLSTKEALDE 693
Qy 227 SLPEVSLILKILKKNDEPFWVLGTLASVLTGTVHPVPSIIIPAKIITMF-GNNDKTTLKH 285
Db 694 SIPPVFWIMKMLNLTENFYVGVFCALINGLQPAFAVIFSKLIGITRNDADATKQ 753
Qy 286 DABIVSMIFVLGVICFVSFMQGLFYGRAGBILTNRLHLPKAFKAVLYODIAWFDEKENS 345
Db 754 NSNLFSLLFLVLGIVSFITPFLQGFPGKAGEIILTKLRVYVFRSMRLQDVNSFDDPKNT 813
Qy 346 TGGTTLTILADIAIOQAGSRIGVLTONATNMGSLVLIISFYKEMTFILISIAPIAV 405
Db 814 TGLTTRLANDAAQVKGAGSRLAIITQNIANLGVIIISLYGQTLTLLLAIVPIAI 873
Qy 406 TGMTIATMTGAFKNDKQELKAGKIATEALENIRTVSLTRKAFQMYEEMLOTHRN 465
Db 874 AGVYEMXLSQALUKDKLEGAGKIATEALENIRTVSLTRKAFQMYEEMLOTHRN 933
Qy 466 TSKAQIIGSCYAFSAFHAFFAYAGFRFGAYLQAGRWTPGEGFIVFTAIAYGAMAIGK 525
Db 934 SLRKAHIFGITFTQAMMYFSAFHAFFAYAGFRFGAYLQAGRWTPGEGFIVFTAIAYGAMAIGK 993
Qy 526 TLVLAPYSKAKSAAHLPALLEKKNIDSRQSGKGPDTCEGNLBRFVSVFFYPCRPDV 585
Db 994 VSSPAPDYAKAKVSAHHIIMIEKPLDYSYSTGLKPLTEGNVTFNEVVFYPTFLDI 1050
Qy 586 FILGSLISIERGKTVAFFVSGSGGKSTVOLLORLYDPVQGVLDGDAKELNVQWLR 645
Db 1054 PVLGSLSEVKKGTLLALVSGSGGKSTVOLLORLYDPVQGVLDGDAKELNVQWLR 1113
Qy 646 SOIAIVPOBPVLPNCSTAEINAYGNSRWVPLDRIKSAANAANIHSFIEGLPEKINTQVG 705
Db 1114 AHLGIVSQEPILFDCSISEINAYGNSRWVQSEIIVRAAKEANIHFIESLPNKYSTRVG 1173
Qy 706 LKGAQLSGGQKORAIARALVQPHILLDEATSDNDSEKVVQHALDKARTGRTCLV 765
Db 1174 DKGTLQSGGQKORAIARALVQPHILLDEATSDNDSEKVVQHALDKARTGRTCLV 1233
Qy 766 THRLSAIQNADLIVVFNHNGKIKEGQTHOBLNRNDIYFKLVNAQS 810
Db 1234 AHRSTIQNADLIVVFNHNGKIKEGQTHOBLNRNDIYFKLVNAQS 1278

RESULT 3

US-09-672-810-7
; Sequence 7, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEINEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-672-810-7

Query Match 59.8%; Score 2438; DB 4; Length 1280;
Best Local Similarity 56.8%; Pred. No. 5.2e-229;

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Matches 467; Conservative 162; Mismatches 178; Indels 18; Gaps 4;
QY 2 VDENDIRALNVRHVRDHIGVWSQEPVLFGTTISNNIKYGRDDVTDEMERARANAAYDF 61
Db IDQDQDRTINVRHRLRITGVVSGEPVLFGTTIAENIRYGRNVNDEIEKAVKEANAYDF 513
QY 62 IMEFPNKNFTLVGKGAQSGGQKORIAIARALVRNPVKILILDEATSLDSSKSAVQAA 121
Db IMKLPNKFDFLVRGARGSLGGQKORIAIARALVRNPVKILILDEATSLDSSKSAVQAA 573
QY 122 LEKASGRTTIVVAHRLSTIRSDLVTLKDGMLAKGAHAELMAKRGILYVSLVMSQDIK 181
Db LDKARKGRTTIVVAHRLSTIRSDLVTLKDGMLAKGAHAELMAKRGILYVSLVMSQDIK 574
QY 182 KADQESMTYSTERKNSLPLHSVKSIDSDEI-----DKAESSTQSKI 226
Db GNEIENATGESKSSDALEM-SPDSGSLIKRSTRSIRHAPQDQKLGKTKEDLNE 691
QY 227 SLPEVLLKILKLNKPWPVVLGTILASVLNGTVHPVFSIIFAKIITMP-GNNDKTTLKH 285
Db NVPSSVFWRLKLNSTWEPVVGIFCAIINGGLQPAFISIFRIIGITFRDSDPTKQ 751
QY 286 DAIYSMIFVLGVI CFVSVFMGCLFYGRAGEILTMRHLRAKAMLYODIAWDEKENS 345
Db NSNMFVFLVGLIISFITFLQGFYGRAGEILTMRHLRAKAMLYODIAWDEKENS 752
QY 346 TGGTLTILADIAIQIAGTSGRISCVLTQNTNMGSLVSIISFYGWEMTFLILSIAPVLAV 405
Db TGTALTFLANDAAQVKAIGSLRAVITQNTNMGSLVSIISFYGWEMTFLILSIAPVLAV 871
QY 406 TGMETRAMTGFANKQKQKHLKAGKATATEALENIRIVSLTRKATPEQWYEMLOTHRN 465
Db AGVEMKMLSGQALDKKKELEGAGKATATEALENIRIVSLTRKATPEQWYEMLOTHRN 872
QY 466 TSKAQIIGSCYAFSAIFVFAAAGFRFGAYLIQAGRWTPEGMFIVFTAIAYGAMAIGK 525
Db SLKAMIFGVSPITQWQYFSAAGFRFGAYLIQAGRWTPEGMFIVFTAIAYGAMAIGK 931
QY 526 TLVLAPYSKAGGAHLFALLEKKNIDRSOEGKKPOTCEGNLSEFVSPYPCRPDV 585
Db VSSFAPDYAKARVSAAHVIMIEKSLIDSYSPHGLKPNLTLEGNVTFVFNVPTRPDI 1051
QY 586 FILRGLSLSTERKNTVAFVSGSCGKSTVQLLORLYDPOGOVLPDGVDAKELNOMLR 645
Db PVQLGLSLVKKQTLALVSGSCGKSTVQLLORLYDPOGOVLPDGVDAKELNOMLR 1111
QY 646 SQIAPVQEPVLFNCISIAENIAYGDSRVVPLDEIKEAANAANIHSFIEGLPEKNTQVG 705
Db AHLGIVSQEPILFDCSIAENIAYGDSRVVPLDEIKEAANAANIHSFIEGLPEKNTQVG 1112
QY 706 LKGAQISGGQKORIAIARALVRNPVKILILDEATSLDSSKSAVQAA 765
Db DKGTQISGGQKORIAIARALVRNPVKILILDEATSLDSSKSAVQAA 1171
QY 766 THRLSAIQNADLTIVLHNGIKQGTQHEILLNRDIYFKLVNAQS 810
Db ARLSTIQNADLTIVLHNGIKQGTQHEILLNRDIYFKLVNAQS 1231

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RESULT 4

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US-08-784-649A-2
; Sequence 2, Application US/08784649A
; Patent No. 5830697
; GENERAL INFORMATION:
; APPLICANT: Siskic, Branimir I
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
; CYCLOSPORIN MODULATION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park

```

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; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,649A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: Reg. No. 5830697 36,677
; REFERENCE/DOCKET NUMBER: 06037/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1279 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-784-649A-2
; Query Match 59.7%; Score 2436; DB 2; Length 1279;
; Best Local Similarity 56.6%; Pred. No. 8.2e-229;
; Matches 466; Conservative 166; Mismatches 177; Indels 14; Gaps 4;
QY 2 VDENDIRALNVRHVRDHIGVWSQEPVLFGTTISNNIKYGRDDVTDEMERARANAAYDF 61
Db IDQDQDRTINVRHRLRITGVVSGEPVLFGTTIAENIRYGRNVNDEIEKAVKEANAYDF 511
QY 62 IMEFPNKNFTLVGKGAQSGGQKORIAIARALVRNPVKILILDEATSLDSSKSAVQAA 121
Db IMKLPNKFDFLVRGARGSLGGQKORIAIARALVRNPVKILILDEATSLDSSKSAVQAA 571
QY 122 LEKASGRTTIVVAHRLSTIRSDLVTLKDGMLAKGAHAELMAKRGILYVSLVMSQ--- 178
Db LDKARKGRTTIVVAHRLSTIRSDLVTLKDGMLAKGAHAELMAKRGILYVSLVMSQ--- 631
QY 179 ---DIKKADEQMESWTYSTERKNSLPLHSV-----KSIK-SDFIDKAESTQSKLSL 228
Db NEVELENADESKSIDALEMSNDSRLKRSSTRSVSGSQADRLSKTKEALDESI 691
QY 229 PEVSLKILKLNKPWPVVLGTILASVLNGTVHPVFSIIFAKIITMPGN-NDKTTLKHDA 287
Db PPVSWRIMKLNLTWEPVVGIFCAIINGGLQPAFISIFRIIGITFRDSDPTKQNS 751
QY 286 EIYSMIFVLGVI CFVSVFMGCLFYGRAGEILTMRHLRAKAMLYODIAWDEKENS 347
Db NLFSLPLALGIISFITFLQGFYGRAGEILTMRHLRAKAMLYODIAWDEKENS 811
QY 348 GTTTLTILADIAIQIAGTSGRISCVLTQNTNMGSLVSIISFYGWEMTFLILSIAPVLAVTG 407
Db ALTFLANDAAQVKAIGSLRAVITQNTNMGSLVSIISFYGWEMTFLILSIAPVLAVTG 871
QY 408 MIETAAMTGFANKQKQKHLKAGKATATEALENIRIVSLTRKATPEQWYEMLOTHRN 467
Db VVEMKMLSGQALDKKKELEGAGKATATEALENIRIVSLTRKATPEQWYEMLOTHRN 931
QY 468 KKAQIIGSCYAFSAIFVFAAAGFRFGAYLIQAGRWTPEGMFIVFTAIAYGAMAIGKTL 527
Db KKAQIIGSCYAFSAIFVFAAAGFRFGAYLIQAGRWTPEGMFIVFTAIAYGAMAIGKTL 931
QY 932 RKAHIFGTTFTQAMTFFSTAGCFRFGAYLIQAGRWTPEGMFIVFTAIAYGAMAIGKTL 587
Db RKAHIFGTTFTQAMTFFSTAGCFRFGAYLIQAGRWTPEGMFIVFTAIAYGAMAIGKTL 1051
QY 588 LRGLSLSTERKNTVAFVSGSCGKSTVQLLORLYDPOGOVLPDGVDAKELNOMLR 647

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Db 1052 LQGLSLEVKGGTALVSSGCGKSTVQLLRFYDPLAGVLDGKEIKELNVQWURAH 1111
Qy 648 IAIVPOEPVLFNCISAEINAYGDSRVPLDEIKEAANAANIHSFIEGLPEKNTVOGLK 707
Db 1112 LGIVSQEPILFDCISAEINAYGDSRVVQSEIVRAAKANIHAIESPLPKYKTVGDK 1171
Qy 708 GAQLSGGQKQRLAARALLOKPKILLDEATSDNDSEKVVQCHALDKARTGRCIVIAH 767
Db 1172 GTQLSGGQKQRIARALVRQPHILLDEATSDNDSEKVVQCHALDKARTGRCIVIAH 1231
Qy 768 RLSAIQNALIVLVHNGKIKQGTTHQELLNRDIYFKLVNAQS 810
Db 1232 RLSTIQNALIVLVHNGKIKQGTTHQELLNRDIYFKLVNAQS 1274
RESULT 5
US-09-672-810-6
; Sequence 6, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEIMEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1279
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-672-810-6
Query Match 59.7%; Score 2436; DB 4; Length 1279;
Best Local Similarity 56.6%; Pred. No. 8.2e-229;
Matches 466; Conservative 166; Mismatches 177; Indels 14; Gaps 4;
Qy 2 VDENDIRALNVRHYRDIHGVVSGEPVLFGTTISNNIKYGRDDVTDDEMERAAEANYDF 61
Db 452 VGGQDRTINVRLEIIGVWSQEPVLFAITIAENIRYGRNVMTDEIKAVKEANYDF 511
Qy 62 IMEFPNKENTLVGKGAQMSGQKQRIARALVRNPKILLDEATSDNDSEKSAVQAA 121
Db 512 IMKLPKHFDTLVGERGAGLSSGQKQRIARALVRNPKILLDEATSDNDSEKSAVQAA 571
Qy 122 LEKASKGRTTIVVAHRLSTIRSDALIVTLKDGMAEKAHAELMAKRGYLYSVMSQ--- 178
Db 572 LDKARKGRTTIVVAHRLSTIRSDALIVTLKDGMAEKAHAELMAKRGYLYSVMSQTAG 631
Qy 179 ---DIKKADEQMSMTYSTERTNSLPLHSV-----KSIIK-SDFIDKAEESTOSKEISL 228
Db 632 NEVELENADESKSDEIDALEMSNDSRLIRKSTRSVRSVGSQQRKLSKEALDESI 691
Qy 229 PEVSLKLIKLNKPEWPFVLGTLASVLNGTVHVPFSTIPIAKIITMFGN-NDKTTLKXDA 287
Db 692 PVSFWRMKLNLTWPYFVGVPCAIINGLQPAFALIPSKIIIGVFTRIIDDPETKQNS 751
Qy 288 EYISMIFVLGVICFVSVPMDGLFVGRAGETLWELRLHAKMLYQDIAMFOKENSTG 347
Db 752 NULFSULFALGLIISITITFLOQFTGKAGEILTKELRVNFRSMRLQVDSWFDOPKNTG 811
Qy 348 GLTTILAIIDIAIQGATSGRIGVLTONATNMGSLVSIISFYIGWMTFILISIAPVLAVTG 407
Db 812 ALTTIRLANDAAQVKGAIGSRSLAVITQNLANTLGITIIISFYIGWQLTLLLAIVPIIAAG 871
Qy 408 MIETAMTGFANKDKQELKHAKGKATEALENIRITVLTREKAFQMTYEMQLQHRNTS 467

Db 872 VDEMRLSQAULKKEKELSGAGKIATEIENFRVVSLSLTQEQKFEHMYAQSLQVFRNSL 931
Qy 468 KKAQIIGSCYAFSHAFIYFAYAGFRFGAYLIQAGRTPEGMFIVFTAIYAGMAIGKTL 527
Db 932 KKAHIFGITISFTQAMWFSYAGCFRFGAYLVAHKLMSFEDVLLVFSAVVFGAMAVQVS 991
Qy 528 VLAPEYKSAKSGAHLFALLEKKNIDSRSQKPKDTCENLREFEVFFVPCRDVFI 587
Db 992 SPAPDFAKAKISAAHIIIEKTFELDSYSTGLMPTLEGNTVFEVFNFTREDIPV 1051
Qy 588 LRGLSLSIBERGKTIVAFVSGSGGCKSTSVQLLQRLYDPVQOVLFDGVDKALENVOLRSQ 647
Db 1052 LQGLSLEVKGGTALVSSGCGKSTVQLLRFYDPLAGVLDGKEIKELNVQWURAH 1111
Qy 648 IAIVPOEPVLFNCISAEINAYGDSRVPLDEIKEAANAANIHSFIEGLPEKNTVOGLK 707
Db 1112 LGIVSQEPILFDCISAEINAYGDSRVVQSEIVRAAKANIHAIESPLPKYKTVGDK 1171
Qy 708 GAQLSGGQKQRIARALLOKPKILLDEATSDNDSEKVVQCHALDKARTGRCIVIAH 767
Db 1172 GTQLSGGQKQRIARALVRQPHILLDEATSDNDSEKVVQCHALDKARTGRCIVIAH 1231
Qy 768 RLSAIQNALIVLVHNGKIKQGTTHQELLNRDIYFKLVNAQS 810
Db 1232 RLSTIQNALIVLVHNGKIKQGTTHQELLNRDIYFKLVNAQS 1274
RESULT 6
US-09-767-594-2
; Sequence 2, Application US/09767594
; Patent No. 6521635
; GENERAL INFORMATION:
; APPLICANT: Bates, Susan
; APPLICANT: Robey, Robert
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Inhibition of MXR Transport by Acridine Derivatives
; FILE REFERENCE: 015280-402100US
; CURRENT APPLICATION NUMBER: US/09/767,594
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/177,410
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human p-glycoprotein (Pgp)/multi-drug resistance 1
; OTHER INFORMATION: (Mdr-1) ATP-binding cassette (ABC transporter)
; OTHER INFORMATION: protein
US-09-767-594-2
Query Match 59.7%; Score 2436; DB 4; Length 1280;
Best Local Similarity 56.6%; Pred. No. 8.2e-229;
Matches 466; Conservative 166; Mismatches 177; Indels 14; Gaps 4;
Qy 2 VDENDIRALNVRHYRDIHGVVSGEPVLFGTTISNNIKYGRDDVTDDEMERAAEANYDF 61
Db 453 VGGQDRTINVRLEIIGVWSQEPVLFAITIAENIRYGRNVMTDEIKAVKEANYDF 512
Qy 62 IMEFPNKENTLVGKGAQMSGQKQRIARALVRNPKILLDEATSDNDSEKSAVQAA 121
Db 513 IMKLPKHFDTLVGERGAGLSSGQKQRIARALVRNPKILLDEATSDNDSEKSAVQAA 572
Qy 122 LEKASKGRTTIVVAHRLSTIRSDALIVTLKDGMAEKAHAELMAKRGYLYSVMSQ--- 178
Db 573 LDKARKGRTTIVVAHRLSTIRSDALIVTLKDGMAEKAHAELMAKRGYLYSVMSQTAG 632
Qy 179 ---DIKKADEQMSMTYSTERTNSLPLHSV-----KSIIK-SDFIDKAEESTOSKEISL 228

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Db 633 NEVELENADESSEIDALEMSNDSSLRKSTRSRVSGSOAQDRKLSKEALDESI 692
Qy 229 PEVSLKILKLNKPEMPFVVLGTLASVNGTVHPVFSIIIPAKIITMFGN-NDKTTLKHDA 287
Db 693 PPSVFWIRIMKLNLTWPYFVGVFCALINGGLQAPAFIIFSKIIIGVTRIDDPETKQNS 752
Qy 288 ELYSMILFVLGVCFSYFNOGLFYGRAGEILTWRLHLPKAMLYODIAWFEKENSTG 347
Db 753 NLFSLFLAUGIISITFIIFLQGTGKAGELITKRLRYWFRSMRLQDVSFDDPKMTTG 812
Qy 348 GLTTLAIDIAIQGATSGRIGVLTQNTATNMGLSVIISFIYGMETPLILSIAPVLAVTG 407
Db 813 ALTRLANDAAQVKAIGSLAVITQNTIANLGTVIISFIYGMQLTLLLLAIVPIAIAG 872
Qy 408 MIETAAMTGFANKQKQELKAGKIATEALENITIVSLTRKAPFQMYEMLTOHRTS 467
Db 873 VWMKMLSGQALKKKKELEGAGKIATEALENITIVSLTRKAPFQMYEMLTOHRTS 932
Qy 468 KKAQIIGSCVAFSHAFIYFAYAGFRFGAYLIQAGRWTPGMEIIVFTAIYAGMAIGKTL 527
Db 933 KKAHIFGITFPTQMMYFSYAGCFRFGAYLVAKHLMSPEDVLLVFSVAVFGMAVGQVS 992
Qy 528 VLAPEYSKAKSGAAHLPALLEKKNIDSRQSGKKPDTCEGNLEPREVFFYPCRPDVFI 587
Db 993 SPAPDYAKAKISAAHIIIMITEKFLIDSYSYTEGLMPNTLEGNTVFGVVFYPTRPDIPV 1052
Qy 588 LRGLSLIERGKTVAFCVSSGCGKSTSVOLLQRLYDPVGOVLFGVDKELNVQWLRSQ 647
Db 1053 LQGLSLVKKQGTALVGGSGCGKSTVQLLEFYDPLAGKVLDDGKSLRLNVQWIRAH 1112
Qy 648 IALVQPEPVLFNCSIAENIAYGDSNRVPLDEIKEAANAANIHSFIIEGLPEKYNTOVGLK 707
Db 1113 LGIVSQEPILFDCSIAENIAYGDSNRVSVQSEIIVRAAKEANIHFIESLPNKYSTKVGDK 1172
Qy 708 GAOLSGGOKORLAIARALLOKPKILLIDRATSLDNDSEKVVQHALDKARTGRTCLVYTH 767
Db 1173 GTQLSGGOKORLAIARALVROPHILLIDRATSLDSEKVVQHALDKARTGRTCLVYTH 1232
Qy 768 RLSAIQNADLIIVLHNGKIKQGTQHELLNRDIYFKLVNAQS 810
Db 1233 RLSTIQNADLIIVFQNGRVEHGHQQLLAQKGIYFSMVVQA 1275
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RESULT 7

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US-09-672-810-5
; Sequence 5, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEINEL-CRESPI, DOROTHY T.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-672-810-5
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Query Match 59.7%; Score 2436; DB 4; Length 1280;
Best Local Similarity 56.6%; Pred. No. 8.2e-229;
Matches 466; Conservative 166; Mismatches 177; Indels 14; Gaps 4;
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Qy 2 VBENDIRALNVRHYRDHIGVWSQSPVLFGTTISNNIKYGRDDVTDENVERAAAEANAYDF 61
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Db 453 VDGQDIRTINVRPLSEIIGVWSQEPVLFATTIAENIRYGRNVTDIEIKAYKEANAYDF 512
Qy 62 IMEFNKNTLVGEGKAGQSGQKQRIARALVRNPKILILDEATSLDSEKSAVQAA 121
Db 513 INKLPHKQDTLVGERGAGLQSGQKQRIARALVRNPKILILDEATSLDSEKSAVQAA 572
Qy 122 LEKASGRTTIVVAHRLSTIRSDILVTLKOGKLABKHAELMAKRGYIYSLVMSQ--- 178
Db 573 LDKAEKGRITTVIAHRLSTVRNADVIAGFDGQVIVEKGNHDELMKEKGIYFKLVMTQTAG 632
Qy 179 ---DIKKADBOEMESMTYSTERTKINSPLPLHSV-----KSIK-SDFIDKAEESTOSKEISL 228
Db 633 NEVELENADESSEIDALEMSNDSSLRKSTRSRVSGSOAQDRKLSKEALDESI 692
Qy 229 PEVSLKILKLNKPEMPFVVLGTLASVNGTVHPVFSIIIPAKIITMFGN-NDKTTLKHDA 287
Db 693 PPSVFWIRIMKLNLTWPYFVGVFCALINGGLQAPAFIIFSKIIIGVTRIDDPETKQNS 752
Qy 288 ELYSMILFVLGVCFSYFNOGLFYGRAGEILTWRLHLPKAMLYODIAWFEKENSTG 347
Db 753 NLFSLFLAUGIISITFIIFLQGTGKAGELITKRLRYWFRSMRLQDVSFDDPKMTTG 812
Qy 348 GLTTLAIDIAIQGATSGRIGVLTQNTATNMGLSVIISFIYGMETPLILSIAPVLAVTG 407
Db 813 ALTRLANDAAQVKAIGSLAVITQNTIANLGTVIISFIYGMQLTLLLLAIVPIAIAG 872
Qy 408 MIETAAMTGFANKQKQELKAGKIATEALENITIVSLTRKAPFQMYEMLTOHRTS 467
Db 873 VWMKMLSGQALKKKKELEGAGKIATEALENITIVSLTRKAPFQMYEMLTOHRTS 932
Qy 468 KKAQIIGSCVAFSHAFIYFAYAGFRFGAYLIQAGRWTPGMEIIVFTAIYAGMAIGKTL 527
Db 933 KKAHIFGITFPTQMMYFSYAGCFRFGAYLVAKHLMSPEDVLLVFSVAVFGMAVGQVS 992
Qy 528 VLAPEYSKAKSGAAHLPALLEKKNIDSRQSGKKPDTCEGNLEPREVFFYPCRPDVFI 587
Db 993 SPAPDYAKAKISAAHIIIMITEKFLIDSYSYTEGLMPNTLEGNTVFGVVFYPTRPDIPV 1052
Qy 588 LRGLSLIERGKTVAFCVSSGCGKSTSVOLLQRLYDPVGOVLFGVDKELNVQWLRSQ 647
Db 1053 LQGLSLVKKQGTALVGGSGCGKSTVQLLEFYDPLAGKVLDDGKSLRLNVQWIRAH 1112
Qy 648 IALVQPEPVLFNCSIAENIAYGDSNRVPLDEIKEAANAANIHSFIIEGLPEKYNTOVGLK 707
Db 1113 LGIVSQEPILFDCSIAENIAYGDSNRVSVQSEIIVRAAKEANIHFIESLPNKYSTKVGDK 1172
Qy 708 GAOLSGGOKORLAIARALLOKPKILLIDRATSLDNDSEKVVQHALDKARTGRTCLVYTH 767
Db 1173 GTQLSGGOKORLAIARALVROPHILLIDRATSLDSEKVVQHALDKARTGRTCLVYTH 1232
Qy 768 RLSAIQNADLIIVLHNGKIKQGTQHELLNRDIYFKLVNAQS 810
Db 1233 RLSTIQNADLIIVFQNGRVEHGHQQLLAQKGIYFSMVVQA 1275
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RESULT 8

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5206352-4
; Patent No. 5206352
; APPLICANT: Robinson, Igor B.; Pastan Ira H.; Gottesman, Michael M.
; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/622,836
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 892,575
; FILING DATE: 01-AUG-1986
; APPLICATION NUMBER: 845,610
; FILING DATE: 28-MAR-1986
; SEQ ID NO:4;
```

LENGTH: 1280

TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
TITLE OF INVENTION: SELECTION OF CELLS TRANSFECTED WITH SUCH GENES

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi & Stewart
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DNA V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,276
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/332,444
FILING DATE: 31-OCT-1994
APPLICATION NUMBER: 07/887,712
FILING DATE: 22-MAY-1992
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1280 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
US-08-583-276-19

Query Match 59.7%; Score 2436; DB 2; Length 1280;
Best Local Similarity 56.6%; Pred. No. 1.3e-228;
Matches 466; Conservative 165; Mismatches 178; Indels 14; Gaps 4;

QY 2 VDENDIRALNVRHYRHDHGVVQSPVLPFGTTISNNIKYGRDDVTDDEMEARAENAYDF 61
DB 453 VDQDQRTINVRFLREIIGVWVQSPVLPFGTTISNNIKYGRDDVTDDEMEARAENAYDF 512
QY 62 IMEFPNFKNTLVCKEKAQMSGGQKQRIATARALVRNPKILLDATSALESKSAVQAA 121
DB 513 IMKLPHKFDLVGERAQLSGGQKQRIATARALVRNPKILLDATSALESKSAVQAA 572
QY 122 LEKASKGRTTIVVAHRLSTIRSDLVTLKQMLAEKGAHAELMAKRGLYSLVMQ--- 178
DB 573 LDKARKGRTTIVIAHRLSTVRNADVTAGDDGVIVKGNHDELMKEKGIYFKLVMTQTAG 632
QY 179 ---DIKKADBOMESMTYSTERTKNSLPLHSV-----KSIK-SDFIDKABESTQSKEISL 228
DB 633 NEVELENAADESKSHDALEMSNDSSRLIRKSTRSVRGSAQDRKLSKTEALDESI 692
QY 229 PEVSLKILKLNKPEMPFVVLGLTASVLNGTTHVHPFSIIIPAKIITMFGN-NDKITLKHDA 287
DB 693 PPVSPWRIMKLNLTENPYPVGVVFCALINGGLQPAFALIFSKIIVFTRIDDPETKQNS 752
QY 288 EIVSMIPVILGVICFVSFMOGLFYGRAGEILTMRLRLHAPKAMLYODIAWFEKENSTG 347
DB 753 NLFSLLFALGIIISPIITFLOQGETFGKAGEILTKRLRYMVRSMKLDQVSWFDDPKNNTG 812
QY 348 GLATTILADIAIQGATGSRIGVLTONATNMGSLVIIISFYIYGNMTPLILISAPVLAVTG 407
DB 813 ALITRLANDAAQVKGAGISRLAVITQNIANGTGIIISFYIYGNMTPLILISAPVLAVTG 872
QY 408 MIETAAMTGPAKQKQELKHAQKIAATEAENITIVSLTREKAFECOMYEMLQTOHNTS 467
DB 873 VVEMKMLSGQALKDQKKELEGAGKIAATEAENITIVSLTREKAFECOMYEMLQTOHNTS 932
QY 468 KKAQILGSCYAFSHAFIYFAYAGFRFGAYLIQAGRWMTPEGMFIVFTAYAGMAIGKTL 527

5206352-4

Query Match 59.7%; Score 2436; DB 6; Length 1280;
Best Local Similarity 56.6%; Pred. No. 8.2e-229;
Matches 466; Conservative 166; Mismatches 177; Indels 14; Gaps 4;

QY 2 VDENDIRALNVRHYRHDHGVVQSPVLPFGTTISNNIKYGRDDVTDDEMEARAENAYDF 61
DB 453 VDQDQRTINVRFLREIIGVWVQSPVLPFGTTISNNIKYGRDDVTDDEMEARAENAYDF 512
QY 62 IMEFPNFKNTLVCKEKAQMSGGQKQRIATARALVRNPKILLDATSALESKSAVQAA 121
DB 513 IMKLPHKFDLVGERAQLSGGQKQRIATARALVRNPKILLDATSALESKSAVQAA 572
QY 122 LEKASKGRTTIVVAHRLSTIRSDLVTLKQMLAEKGAHAELMAKRGLYSLVMQ--- 178
DB 573 LDKARKGRTTIVIAHRLSTVRNADVTAGDDGVIVKGNHDELMKEKGIYFKLVMTQTAG 632
QY 179 ---DIKKADBOMESMTYSTERTKNSLPLHSV-----KSIK-SDFIDKABESTQSKEISL 228
DB 633 NEVELENAADESKSHDALEMSNDSSRLIRKSTRSVRGSAQDRKLSKTEALDESI 692
QY 229 PEVSLKILKLNKPEMPFVVLGLTASVLNGTTHVHPFSIIIPAKIITMFGN-NDKITLKHDA 287
DB 693 PPVSPWRIMKLNLTENPYPVGVVFCALINGGLQPAFALIFSKIIVFTRIDDPETKQNS 752
QY 288 EIVSMIPVILGVICFVSFMOGLFYGRAGEILTMRLRLHAPKAMLYODIAWFEKENSTG 347
DB 753 NLFSLLFALGIIISPIITFLOQGETFGKAGEILTKRLRYMVRSMKLDQVSWFDDPKNNTG 812
QY 348 GLTTILADIAIQGATGSRIGVLTONATNMGSLVIIISFYIYGNMTPLILISAPVLAVTG 407
DB 813 ALITRLANDAAQVKGAGISRLAVITQNIANGTGIIISFYIYGNMTPLILISAPVLAVTG 872
QY 408 MIETAAMTGPAKQKQELKHAQKIAATEAENITIVSLTREKAFECOMYEMLQTOHNTS 467
DB 873 VVEMKMLSGQALKDQKKELEGAGKIAATEAENITIVSLTREKAFECOMYEMLQTOHNTS 932
QY 468 KKAQILGSCYAFSHAFIYFAYAGFRFGAYLIQAGRWMTPEGMFIVFTAYAGMAIGKTL 527
DB 933 RKAHIFGITTSFTQAMTFVSAGCPFGAYLVAKHLMSEFDVLLVFSAVVFGMAVQVS 992
QY 528 VLAPYSKAKGAHLFALLEKKNIDSRQEKKPDCEGNLSRVSFVPCBPVFI 587
DB 993 SPAPDYAKAKISAHHIIMIKTPLIDISTEGLMPTLEGNVTFGVVFNPTRPDIPV 1052
QY 588 LRGLSLIERGKTVAFVSSGCGKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQMLRSQ 647
DB 1053 LQGLSLVKKGTALVSSGCGKSTSVQLLQRLYDPVQGVLPDGVDAKELNVQMLRAH 1112
QY 648 TAVDQEPVLPNCSTAEINAYGDSRVVPLDEIKEAANAHHISFIEGLPEKNTVGLK 707
DB 1113 LGVISOEPILFDCSIAENIAYGDSRVVQBEIVRAAKAENIHAIFESLPNKYSTKVGDK 1172
QY 708 GAQLSGGQKQRIATARALQKPKILLDEATSALENDSEKVVQVQALDKARTGRTCLVVTH 767
DB 1173 GTQLSGGQKQRIATARALVRQPHILLDEATSALENDSEKVVQVQALDKAREGRICIVIAH 1232
QY 768 RLSTATONADLIVLHNGKIKGQTHQELLNRNDYFKLVNAQS 810
DB 1233 RLSTIQNADLIVFQNGRVKRGHTHQQLLAQKGIYFSMVSVQA 1275

RESULT 9
US-08-583-276-19
Sequence 19, Application US/08583276
Patent No. 5837536
GENERAL INFORMATION:
APPLICANT: McDonagh, Kevin T.
APPLICANT: Nienhuys, Arthur
APPLICANT: Tolcoshev, Paul
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN

933 RKAHIFGTFSTQAMMYFAGCFRFGAYLVAKHLMSPEDVILLVFSVAVFGAMVQVS 992
 528 VLAPYKAKSGAHLFALEKXPNIDSRQEGKPKDTCGNLEFREVFFYPCRDVFI 587
 993 SPAPDAKAKISAHHIIMIEKPLDLSYSTGLMENTLEGNTFGEVWNYTRDIPV 1052
 588 LRLSLSIERGKTVAFVGGSGGCKSTVQLLQRLYDPVQGVLPFGVDKAKELNVQMLRSQ 647
 1053 LQGLSLEVKKGQTLALVGGSGGCKSTVQGLERFYDPLAGKVLDDGKBIKRLNVQMLRAH 1112
 648 IATVQEPVLPNCISAIENIAYGNSRVVPLDEIKKAAANAIIHSPFIEGLPEKYNTOVGLK 707
 1113 LGIVSQEPILFDCSIAENIAYGNSRVVQEEIVRAKEANIIPFIESLPKSTKVGDK 1172
 708 GAOLSGGQKORLAIARALLQPKILLDEATSDALDNDSEKVVQHALDKARTGRTCLVWTH 767
 1173 GTQLSGGQKORLAIARALVQPHILLDEATSDALDNDSEKVVQBALDKAREGRTCIIVAH 1232
 768 RLSAIONADLIVLVHNGKIKKQTHQELLRNRIYFKLVNAQS 810
 1233 RLSTIONADLIVVQNGRVEHGHQOQLLAQKGIYFSWVQ 1275
 RESULT 10
 US-09-120-513-2
 ; Sequence 2, Application US/09120513
 ; Patent No. 6025160
 ; GENERAL INFORMATION:
 ; APPLICANT: Brum, Kimberly
 ; APPLICANT: Chenery, Richard
 ; APPLICANT: Ellens, Harma
 ; APPLICANT: Field, John
 ; APPLICANT: Yue, Lin
 ; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE
 ; TITLE OF INVENTION: SEQUENCES ENCODING RAT MDR1B2 AND
 ; TITLE OF INVENTION: SCREENING METHODS THEREOF
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Smithline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/120.513
 ; FILING DATE: 22-JUL-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: King, William T
 ; REGISTRATION NUMBER: 30,954
 ; REFERENCE/DOCKET NUMBER: GP50008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-270-5015
 ; TELEFAX: 610-270-5090
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1275 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-120-513-2
 Query Match 59.2%; Score 2413.5; DB 3; Length 1275;
 Best Local Similarity 56.8%; Pred. No. 1.3e-226;
 Matches 467; Conservative 158; Mismatches 180; Indels 17; Gaps 5;

2 VDENDIRALNVHRDHIGVWSQEPVLFCTTISNNIKYGRDDVDTEEMERAREANAYDF 61
 451 IDQDRTINVTYREILIGVWSQEPVLFATTAENIRYGRNTVMDIEKAVKENAYDF 510
 62 INEFPKNTLVCEKGAQSGGCKORLAIARALVNPXKILIDGATSDALDSEKSAVQAA 121
 511 INKLPKNTLVCEKGAQSGGCKORLAIARALVNPXKILIDGATSDALDSEKSAVQAA 570
 122 LEKASKGRTTIVVHRLSTIRSDILVTLDKGMKAEKGAHAEKMAKRGYLYSLVMSQDIK 181
 571 LKAREGRTTIVIAHRLSTVRNADVAGDGVIVQGNHNEELMKKGIYFPLVMTQ-TR 629
 182 KADEQESMTYTERKTNLSPLHSVKSIDSDFDKA-----BESTOSKE---IS 227
 630 GNEIEPNNAYESQSDTGASELTSEKS-KSPILIRSRIRSRHRODQERRLSKEDVDD 688
 228 LPEVSLKILKLNKPEWPFVVLGTSLASVLNGTVHVFSTIIFAKIITMFG-NNDKTLKHD 286
 689 VPMVSPWQILKLNISEMPVVLVGVLCVINGCIQPVFAIVFSKIVGVPSRDDHETKQKN 748
 287 AEIYSMIFVLGVICFVSFMQGLFYGRAGEILTWRHLHLAFKAMLYQDIAHDEKENST 346
 749 CNLFSLLFLVMGMBISFVTFPQGFPGKAGEILTRELRYVMVFKSMURQDISWDFDHKNT 808
 347 GGLTTILAJDIAQIGATSGRIGVLTONTNMGSLVSIISPIYCWEMTFILSIAPVLAVT 406
 809 GSLTTLASDASNVKSGSLAVTVQNVANLGTGILSLVYGWQLTLLVILVILVILG 868
 407 GMIETAMTFANQKQELKHAKIATEALENIRIVSLTRKAPQOMTEMLQTHNT 466
 869 GIIEMKLLSQALKDKKLEISKIAEIAENFRTVSLTREKQETMYAQSILQIPYRNA 928
 467 SKKAQIIGSCYAFSAFIYFAYAAAGFRFGAYLIQAGMTPEGMFIVFTALVAGMAIGKT 526
 929 LKARVFGITPAFTQMIYFSAACFRFGAYLVARELMTFENVVLVFSVAVFGAMAGNT 988
 527 LVLAPEYSKAKSGAHLFALLEKXPNIDSRQEGKPKDTCGNLEFREVFFYPCRPDVF 586
 989 SSPAPDAKAKYSASHIIRIEKIPEIDSYSTGLKPNLGNVKNVGVNFYPTSPNIP 1048
 587 ILRLSLSIERGKTVAFVGGSGGCKSTVQLLQRLYDPVQGVLPFGVDKAKELNVQWLS 646
 1049 VLOGLSFEVKGQTLVGVSGGCKSTVQGLERFYFYNFAGTVFELDGKBIKQLNVQWLS 1108
 647 QIAIVPQEPVLPNCISAIENIAYGNSRVVPLDEIKKAAANAIIHSPFIEGLPEKYNTOVGL 706
 1109 HLGVSQEPILFDCSITENIAYGNSRVVSHHEIVRAKEANIIPFIESLPKYNTRVGD 1168
 707 KGAOLSGGQKORLAIARALLQPKILLDEATSDALDNDSEKVVQHALDKARTGRTCIIVT 766
 1169 KGTQLSGGQKORLAIARALVQPHILLDEATSDALDSEKVVQBALDKAREGRTCIIV 1228
 767 HRLSAIONADLIVLVHNGKIKKQTHQELLRNRIYFKLVNA 808
 1229 HRLSTIONADLIVVQNGRVEHGHQOQLLAQKGIYFSWVQ 1270
 RESULT 11
 US-09-450-105-2
 ; Sequence 2, Application US/09450105
 ; Patent No. 6163166
 ; GENERAL INFORMATION:
 ; APPLICANT: Kimberly Anne Brum
 ; APPLICANT: Richard James Chenery
 ; APPLICANT: Harma Ellens
 ; APPLICANT: John Anthony Feild
 ; APPLICANT: Lin Yue
 ; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES
 ; TITLE OF INVENTION: ENCODING RAT MDR1B2 AND SCREENING METHODS THEREOF
 ; FILE REFERENCE: GP-50008-D1
 ; CURRENT APPLICATION NUMBER: US/09/450.105
 ; CURRENT FILING DATE: 1999-11-29

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; EARLIER APPLICATION NUMBER: 09/120,513
; EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1275
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-450-105-2

Query Match      59.1%; Score 2412.5; DB 3; Length 1275;
Best Local Similarity 56.1%; Pred. No. 1.8e-226;
Matches 467; Conservative 158; Mismatches 180; Indels 17; Gaps 5;

QY 2 VDENDIRALNVRYHDHGVVSGQVPLFGTTISNNIKYGRDDVTDDEMERAAAEANAYDF 61
DB 451 IDGQDIRTINRYREIIGVWSQEPVLPATTIAENIRYGRNVTDDEIKAVGANAYDF 510
QY 62 IMEPPNKENTLVGKGAQSGGQKQRIATARALVRNPXKILILDEATSDALDSKSAVQAA 121
DB 511 IMKLPHKPTLVGERGAQLSGGQKQRIATARALVRNPXKILILDEATSDALDSKSAVQAA 570
QY 122 LEKASKGRTTIVVAHRLSTIRSDLIIVTLKGMKAEKGAHAELMAKRGLYYSVMSQDIK 181
DB 571 LDKAREGRTTIVIAHRLSTIRSDLIIVTLKGMKAEKGAHAELMAKRGLYYSVMSQDIK 629
QY 182 NADQESMTYSTERTKNSLPLHSVSKTSKDFIDKA-----ESTQSK-----IS 227
DB 630 GNEIPEGNNAVESQSDTGAELTSEKS-KSPLIRSRISIRSHRQDQERRLSKEDVDED 688
QY 228 LPEVLLKILKLNKEPFWVGLTSLVNGTVTPVPSIIIFAKITWFG-NDKXITLKH 286
DB 689 VPMVSFWQLKLNISEMPYLVGVLCVINGCIQVFAIVFSKIVGVFSRDDHSTKQRN 748
QY 287 ABYISMIIVILGVICFVSFVWGQVPGYGRAGELTMRLEHLAFKAMLYODIAWFOBKENST 346
DB 749 CNLFSLLFLVGMISFVTPFGQTFGRAGEILTKRLRYWFKSMLRQDISFDDHNTT 808
QY 347 GGLATILAIIDIAIQGATGSRIGVLTQNTAMGLSVIISFYIYGMETFLILSIAPLAVT 406
DB 809 GSLATRLASDASNVKAGMSRLAVTVQNVANLGTGILSLVGVQWLTLLVVIPLVIG 868
QY 407 GMIETAAMTGKANKDKQLKHAGKIATALENIRITVSLTREKAPQVQVEMLTQRENT 466
DB 869 GIEMKLSGQKDKKQKLEISGKIATEIENFRTVSVLTREKQFETWYASLOIPYANA 928
QY 467 SKKQIIGSCYAFSHAFIYFAYAGFRFGAYLIOAGRMTPGCMFTIVFTAIAYGAMAIGT 526
DB 929 LKKAHVFGITPAFTQAMIVFSYAACFRFGAYLVARELMTFENVMVLPVSAVVFAGAAAGT 988
QY 527 LVLAPEYSKAGSAHLFALLKKNIDRSQEGKQDTCENLEFREVSPFYCRDVP 586
DB 989 SSFADPYAKVSAASHIIRIEKIPEIDSYSTEGKAPNWLGNVAKFNGVMFNYPRNP 1048
QY 587 ILRGLSLSTERGKTVAFVSGSGCGKSTSVQLLRLYDPVQGVLPDGVDAKELNVQMLRS 646
DB 1049 VLQGLSPFVKKGQTLRLVSGSGCGKSTVQLLRLYDPVQGVLPDGVDAKELNVQMLRA 1108
QY 647 QIAIVQBPVLPNCISAIENIAYGDSRVVPLDEIKERANANIHSPFICLPEKNTQVGL 706
DB 1109 HLGVISQBPILFDCSITENIAYGDSRVVSHIEIVRAAREANIHQFIDSLPEKNTRVGD 1168
QY 707 KGAQLSGGQKQRIATARALLOKPKILLDEATSDALDSKSAVQAAKRGYYSVMSQDIK 766
DB 1169 KGTQLSGGQKQRIATARALVRNPXKILILDEATSDALDSKSAVQAAKRGYYSVMSQDIK 1228
QY 767 HRLSAIONADLIVLHNGKIEQGGTHQBELNRDIYFKLVNA 808
DB 1229 HRLSTIONADLIVLHNGKIEQGGTHQBELNRDIYFKLVNA 1270

RESULT 12
US-08-752-447-2

```

```

; Sequence 2, Application US/08752447
; Patent No. 5994088
; GENERAL INFORMATION:
; APPLICANT: Mechetner, Eugene
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Methods and Reagents for Preparing and
; TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSES: McDonnell Boenhen Hulbert & Berghoff Ltd.
; STREET: 300 South Wacker Drive, Seventh Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,447
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5994088nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 95,1121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-9808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-447-2

Query Match      59.1%; Score 2412; DB 2; Length 1280;
Best Local Similarity 56.1%; Pred. No. 1.8e-226;
Matches 462; Conservative 164; Mismatches 183; Indels 14; Gaps 4;

QY 2 VDENDIRALNVRYHDHGVVSGQVPLFGTTISNNIKYGRDDVTDDEMERAAAEANAYDF 61
DB 453 VDQDIRTINRYREIIGVWSQEPVLPATTIAENIRYGRNVTDDEIKAVGANAYDF 512
QY 62 IMEPPNKENTLVGKGAQSGGQKQRIATARALVRNPXKILILDEATSDALDSKSAVQAA 121
DB 513 IMKLPHKPTLVGERGAQLSGGQKQRIATARALVRNPXKILILDEATSDALDSKSAVQAA 572
QY 122 LEKASKGRTTIVVAHRLSTIRSDLIIVTLKGMKAEKGAHAELMAKRGLYYSVMSQDIK 178
DB 573 LDKAREGRTTIVIAHRLSTIRSDLIIVTLKGMKAEKGAHAELMAKRGLYYSVMSQDIK 632
QY 179 ---DIXKADQESMTYSTERTKNSLPLHSV-----KSIKDFIDKAEEST-OSKEISL 228
DB 633 NEVELENADESSEIDALEMSSNDSRSSLIIRKSTERSVRGSAQKRLSTKEALDESI 692
QY 229 PIVSLKILKLNKEPFWVGLTSLVNGTVTPVPSIIIFAKITWFG-NDKXITLKHDA 287
DB 693 PPVSVFRIMKLNLTWPYFVGVFCFVGVFCFVGVFCFVGVFCFVGVFCFVGVFCFVGVFCFV 752
QY 288 EIVSMIFVILGVICFVSFVWGQVPGYGRAGELTMRLEHLAFKAMLYODIAWFOBKENST 347
DB 753 NLFSLFLALGIISFTFFLQGTFFKAGEILTKRLRYWFKSMLRQDISFDDHNTT 812
QY 348 GLTTLIAIDIAIQGATGSRIGVLTQNTAMGLSVIISFYIYGMETFLILSIAPLAVT 407
DB 813 ALITRLANDAAQVKGAGISRLAVITONIANLGTGLIISFYIYGMETFLILSIAPLAVT 872
QY 408 MIETAAMTGKANKDKQLKHAGKIATALENIRITVSLTREKAPQVQVEMLTQRENTS 467

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Db 873 VVENKMPAGQALDKDKELEGAGKIATEAENFRVTVSLTQEQKEHMYAQSLOQVYRNSL 932
 Qy 468 KKAQIIIGSCYAFSHAFTYFAYAGCFREGAYLIQAGRMTPGEMIVFTAIAYGAWAIGKTL 527
 Db 933 KKAHIFGITSFTQAMVFSYAGCFREGAYLVAHKLMSFEDVLLVFSVAVFGMAVQVS 992
 Qy 528 VLAPEYSKAKSGAHLFALLKPKNDISRSQBGKPDTCGNLEFRVSVFFYPCRPDVFI 587
 Db 993 SFAPDYAKAKISAHHIIMEIKTEPLIDSYSTEGMLNTEGNTFGEVWVNYFTREDIPV 1052
 Qy 588 LRGLSISIERGKTVAFYGGSGGCKSTSVOLLQRLYDPVQGVLFQVDAKELAVOMLRSQ 647
 Db 1053 LQGLSLEVKKGQTLALVGGSSGCKSTVQLLEFYDPLAGKVLDDGKEIKELNVQWLEH 1112
 Qy 648 IAIVPOEPVLNCSIAENIAYGNSRVVPLDETEKEAANAANIHSFIEGLPEKYNTOVGLK 707
 Db 1113 LGIVSQEPILFDCSIAENIAYGNSRVVQSEIIVRAAKEANIEAFIESLPNKYSTKVGDK 1172
 Qy 708 GAOLSGGOKORIAARALLQPKILLDEATSDALDSEKVOHAKDKARTGTCLVVT 767
 Db 1173 GTQLSGGOKORIAARLVQPHILLDEATSDALDSEKVOHAKDKAREGRTCTIVIAH 1232
 Qy 768 RLISAIONADLIVLHNGKIKEQOQTHOELLNRDIYFKLVNAQS 810
 Db 1233 RLSTIQNADLIVVFQNGRVEKHGTHOQLLAKQGIYFSMVSVQA 1275

RESULT 13

US-09-316-167-2
 ; Sequence 2, Application US/09316167
 ; Patent No. 6365357
 ; GENERAL INFORMATION:
 ; APPLICANT: Mechetner, Eugene
 ; APPLICANT: Roninson, Igor B
 ; TITLE OF INVENTION: Methods and Reagents for Preparing and
 ; TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff Ltd.
 ; STREET: 300 South Wacker Drive, Seventh Floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: US/09/316,167
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/752,447
 ; FILING DATE: 15-NOV-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6365357nan, Kevin E
 ; REGISTRATION NUMBER: 35,303
 ; REFERENCE/DOCKET NUMBER: 95,1121
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-913-0001
 ; TELEFAX: 312-913-9808
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1280 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-316-167-2

Query Match 59.1%; Score 2412; DB 4; Length 1280;
 Best Local Similarity 56.1%; Pred. No. 1.8e-226;

Matches 462; Conservative 164; Mismatches 183; Indels 14; Gaps 4;
 Qy 2 VBENDIRALNVHRDHIGVVSQEPVLTGTTTNNIKYGGDDVTDDEMERARANAYDF 61
 Db 453 VQODIRITNVPLREIIGVVSQEPVLTGTTTNNIKYGGDDVTDDEMERARANAYDF 512
 Qy 62 IMEFPNKNFTLVGERGAQMSGGOKORIAARALVRNPKILLDEATSDALDSEKSAVQA 121
 Db 513 IMKLPHKFTLVGERGAQMSGGOKORIAARALVRNPKILLDEATSDALDSEKSAVQA 572
 Qy 122 LEKASKGRTTIVVNRHLSITRSADLIVLTKDGLAEKGAHSLMAKRGVLSYVMSQ--- 178
 Db 573 LOKARKGRTTIVVNRHLSITRSADLIVLTKDGLAEKGAHSLMAKRGVLSYVMSQ--- 632
 Qy 179 ---DIKKADEQMESMTYSTERTNSLPLHSV-----KSIKDFIDKABEST-QSKEISL 228
 Db 633 NEVELENAADESKSEIDALEMSSNDSRSLIKRSTRSRVSGSQACHRKLSTKEALDESI 692
 Qy 229 PVSULLKILKLNKPWPVLTGLASVINGTVHPVPSIFAKIITMFGN-NKDTILKHA 287
 Db 693 PVSFWIRKMLNLTWPVWVFGVCAIINGGQPPAFIIFSKIIGVFTRIDPETHKQNS 752
 Qy 288 EYISIMFIVLGVICVSVFMQGLFYGRAGEILTMRLHLAFKAMLYQDIAWFEKENSTG 347
 Db 753 NLFSLLELALGIIISITFTLQSTFTGKAGEILTKELRYMFRSMLRQDYSVHDPKNTTG 812
 Qy 348 GLTTIADIAIQIQTGATSGRIGVLTQNTATNMGLSVIISFIYQWMTFELLSIAPLAVTG 407
 Db 813 ALTTRLANDAAQVGAIGSLAVITQNTANLTGIIISFIYQWMTFELLSIAPLAVTG 872
 Qy 408 MIETAAMTGFANKQKQELKHAGKIATEALENIRTVSLTREKAFBOMTEMLQTOHRNTS 467
 Db 873 VVEMKPFAGQALKDKKELEGAGKIATEAENFRVTVSLTQEQKEHMYAQSLOVYRNSL 932
 Qy 468 KKAQIIIGSCYAFSHAFTYFAYAGCFREGAYLIQAGRMTPGEMIVFTAIAYGAWAIGKTL 527
 Db 933 KKAHIFGITSFTQAMVFSYAGCFREGAYLVAHKLMSFEDVLLVFSVAVFGMAVQVS 992
 Qy 528 VLAPEYSKAKSGAHLFALLKPKNDISRSQBGKPDTCGNLEFRVSVFFYPCRPDVFI 587
 Db 993 SFAPDYAKAKISAHHIIMEIKTEPLIDSYSTEGMLNTEGNTFGEVWVNYFTREDIPV 1052
 Qy 588 LRGLSISIERGKTVAFYGGSGGCKSTSVOLLQRLYDPVQGVLFQVDAKELNVQWLEH 1112
 Db 1053 LQGLSLEVKKGQTLALVGGSSGCKSTVQLLEFYDPLAGKVLDDGKEIKELNVQWLEH 1172
 Qy 648 IAIVPOEPVLNCSIAENIAYGNSRVVPLDETEKEAANAANIHSFIEGLPEKYNTOVGLK 707
 Db 1113 LGIVSQEPILFDCSIAENIAYGNSRVVQSEIIVRAAKEANIEAFIESLPNKYSTKVGDK 1172
 Qy 708 GAOLSGGOKORIAARALLQPKILLDEATSDALDSEKVOHAKDKARTGTCLVVT 767
 Db 1173 GTQLSGGOKORIAARLVQPHILLDEATSDALDSEKVOHAKDKAREGRTCTIVIAH 1232
 Qy 768 RLISAIONADLIVLHNGKIKEQOQTHOELLNRDIYFKLVNAQS 810
 Db 1233 RLSTIQNADLIVVFQNGRVEKHGTHOQLLAKQGIYFSMVSVQA 1275

RESULT 14

US-09-397-233-2
 ; Sequence 2, Application US/09397233
 ; Patent No. 6630327
 ; GENERAL INFORMATION:
 ; APPLICANT: Mechetner, Eugene
 ; APPLICANT: Roninson, Igor B
 ; TITLE OF INVENTION: Methods and Reagents for Preparing and
 ; TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
 ; STREET: 300 South Wacker Drive
 ; CITY: Chicago

STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Skatrud, Paul L.
APPLICANT: de Waard, Maarten A.
APPLICANT: Peery, Robert B.
APPLICANT: Andrade, Alan C.
TITLE OF INVENTION: Multiple Drug Resistance Gene at/d of
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: U.S.
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,545
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-11766
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEFAX: 317-276-2763
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1334 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-545-2

Query Match 41.4%; Score 1690.5; DB 2; Length 1334;
Best Local Similarity 43.5%; Pred. No. 98-156;
Matches 366; Conservative 152; Mismatches 293; Indels 31; Gaps 7;

1 MYDENDIRALNVRHYRDHIGVVSQBPVLFGTTISNNIKYG-----RDDVTDDEMER 51
489 LLDGHDIDLNLRLWLRQQLSLVSQBPVLFGTTIYKNIHGLIGTKYENESSEKVRLEIN 548
52 AREANAYDFIMEPPNKENTLVGEKGAQMSGGQKORIAIARALVNPKNILIDEATSALD 111
549 AARMANAHDFITALEPEGYETNVGQRFLLSGGQKORIAIARAVWSDPKILLDEATSALD 608
112 SSKSAVOAALSKASKGRITIVVAHRLSTIRSDILVTLKQGLMAEKGAHAEIMAKRGILY 171

US-09-397-233-2

Query Match 59.1%; Score 2412; DB 4; Length 1280;
Best Local Similarity 56.1%; Pred. No. 1.8e-226;
Matches 462; Conservative 164; Mismatches 183; Indels 14; Gaps 4;

2 VDENDIRALNVRHYRDHIGVVSQBPVLFGTTISNNIKYGRDDVTDDEMERAREANAYDF 61
453 VDGQDIRTNVRLREIIGVVSQBPVLFGTTIAENIRYGRNVMTDIEKAVKEANAYDF 512
62 IMEPENKENTLVGEKGAQMSGGQKORIAIARALVNPKNILIDEATSALDSEKSAVOAA 121
513 IMKLPKFDTLVGERGALSGGQKORIAIARALVNPKNILIDEATSALDSEKSAVOAA 572
122 LEKASKGRITIVVAHRLSTIRSDILVTLKQGLMAEKGAHAEIMAKRGILYSLVMSQ-- 178
573 LDKARKGRITIVVAHRLSTIRSDILVTLKQGLMAEKGAHAEIMAKRGILYSLVMSQ-- 632
179 ---DIKKADEQMSYSTERKTNLSPLHSV-----KSIKSFIDKABEST-OSKEISL 228
633 NEVELENAADSKSEIDALEMSNDSRLRKSTRSVRGSOAQRKLUKSTKEALDESI 692
229 PEVSLLKILKLNKPEWPFVVLGTLASVLNGTVHPVPSIIFAKIITMFGN-NDKTTLLKHA 287
693 PPVSFWIRKMLNTEWYFVVGVCALINGQLQAPALIFSKLIGVTRIDDPETKQNS 752
288 EISWIFVILGVCISYFMQGLFYGRAGEILLTWRHLAFKAMLYQDIAMFDEKENSTG 347
753 NLFSLFLALGIIISFITPFLQGFTEGKAGEILLTKRLRYMVFMSRLQDVSWFHPDKNTG 812
348 GLTITLADIAIQAGTSGRIGVLTONTATNGLSVIISFYIGEMTFLILSIAPVLAVTG 407
813 ALTTRELANDAAQVKAIGSLRAVLTQNTANLGTGIIISFYIGWQLTLLALLAIPIALAG 872
408 MIEYAMTGFANKQKQELKHAGKIATBALENIRTVSLTREKAPQWYEMLOQCHNTS 467
873 VVEMKMPAGALKKKKELEGAKIATEAENFTVWSLTQEQKPEHYAQSLOQVPYENSL 932
468 KKAQIGSCYAFSAFYFAAGFRGAYLIQAGRVTPGCMPTVFTAIYAGMAIGKTL 527
933 KKAHIFGTFTQMMYFVAGCFRGAYLVAKLMSFEDVLLVFSVAVFGMAVGQNS 992
528 VLAPEYKAKSAAHLLFALLEKZNIDRSQEGKKPDTCRGNLEFREVSVFFYCRPDVFI 587
993 SFAPDYKAKISAAHILMIIEKTLIDISYSTEGLMPNTLEGNVTFGEVWFNYTRPDIPV 1052
588 LRGLSLSTERCKTVAFVSGSSCGKSTSVQLLQRLYDPVQGVLPFGVDKELNVLQRLSQ 647

Db 609 TKSEGVVQALERAAGRTTIVIAHRLSTIKTAHNIWLVNGKIAOQGTDELVDGRGAY 668
Qy 172 YSLVMSQDIKKADEOMESMTYSTERKTN--LPLSHSVKSIKDF-----IDK--AEEST 221
Db 669 RLIVEACRINEOEKAEADADAEADITNADIAKIKTASSASSDLCKPTIDORTGTHKSV 728
Qy 222 QSKBIS-----LPEVSLMLK-----LNKPEPPFVVLGTLASVNGTVHPVFSIIFAKI 271
Db 729 SSAILSKRPPEITPKYSMTLLKLFVAFNRPPEIPYMLIGLVFSLAGGGQPTQAVLYAKA 788
Qy 272 ITWFG--NNDKTTLKHDAEIVSMFVILGVICFVSFVMOGLFYGRAGEILTWRLRHLAFK 329
Db 789 ISTLSLPESQYSLRHADAFWSLXFFVVGIIQITOSTNGAFAVCSERLIRARSTAFR 848
Qy 330 AMLYQDIAMPDENSTGGTLTILADIAQIOGATSGRIGVLTONATNMGLSVIISPIYG 389
Db 849 TILRODIAFDEKENSTGALTSFSTETKHLSCVSGVTLGTILMTSTLGAIIIALAIG 908
Qy 390 WEMTPELILSTAPVLAVTGMTETAAMTGFANKQOELKHAGKIAATEALENIRIVSUTREK 449
Db 909 WKALVCISVVPVLLACGFYRFYMLAQFQSRSLAYEGSANFACEATSSIRIVASLTER 968
Qy 450 AFQMYEMLQTOHRNTSKAQIIGSCYAPSHAFIYFAYAAAGFRFGAYLIOAGRMTPGOM 509
Db 969 DVWEIVHAQDLDAQRTSLISVLSRSLLYASSQALVFFCVAGLGFYGGTLLGHEHYDIFRP 1028
Qy 510 FIVETAIAICAMAIKGTLLVLAPEYSKAKSAAHLFALLEKKPNIDSRQSGKPKDTCGN 569
Db 1029 FVCFSEILFQAQAGTVFSTFAPDMGKAKNAAEFRLEFRKPKPOIDNWSSEGEKLETVGE 1088
Qy 570 LEPREVSFFPCRPDVFILRGLSLSIERGKTVAFVSGSGCGKSTSVQLLQRLYDPVQGV 629
Db 1089 IEFNVHFRYPTREPOVLRGLDITVKPGYVALVSGSGCGKSTTALLERFYDAIAGSI 1148
Qy 630 LFGVDKAKHNVQWLSQTAIVPOEPVLPNCSTAEINIYGDNSRVVPLDEIKEANAANI 689
Db 1149 LVDGKOISKLININSYFSLVSQEPFLYQGTIKENILLGIVEDDVPEBFLIKACKDANI 1208
Qy 690 HSEIQLPEKYNTOVGLKGQKQKORLAIARALLQKPKILLDEATSAIDNDSEKVV 749
Db 1209 YDFIMSLPEGFNTVWSKGMLSGGQKQVARIARALLRDPKILLDEATSAIDSEKVV 1268
Qy 750 QHALDKARTGRTCLVYVTHRLSAIONADLIIVLHNGKIKSQGTHQBELLRNRDIYFKLVNAQ 809
Db 1269 QAALDAAARGRTTIAVAHRLSTIQKADVIYVFDQKIVESGTHSELVQKKGRYVELVNLQ 1328
Qy 810 SV 811
Db 1329 SL 1330

Search completed: June 24, 2004, 15:22:36
Job time : 26 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 25, 2004, 01:23:03 ; Search time 877 Seconds

(without alignments)
4241.556 Million cell updates/sec

Title: US-09-873-409-2
Perfect score: 4079
Sequence: 1 WVDENDIRALNRVHYRDHIG.....QELLNRDIYFKLVNAQSVQ 812

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Database : Published Applications NA:
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19: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description

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2	4079	100.0	3177	9	US-09-873-409-12	Sequence 12, Appl
3	4079	100.0	3621	9	US-09-873-409-14	Sequence 14, Appl
4	4079	100.0	3702	9	US-09-873-409-13	Sequence 13, Appl
5	3919	96.1	3699	16	US-10-415-378-34	Sequence 34, Appl
6	3456	84.7	2066	9	US-09-873-409-9	Sequence 9, Appl
7	3168.5	77.7	4091	13	US-10-032-900A-303	Sequence 303, App
8	2465.5	60.4	3825	17	US-10-383-112-48	Sequence 48, Appl
9	2465.5	60.4	3924	9	US-09-880-107-2299	Sequence 2299, Ap
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15	2441	59.8	4425	9	US-09-769-097-3	Sequence 3, Appl
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17	2436	59.7	3860	9	US-09-866-866A-1	Sequence 1, Appl
18	2436	59.7	3860	9	US-09-866-866A-3	Sequence 3, Appl
19	2436	59.7	4533	13	US-09-805-020-30	Sequence 30, Appl
20	2436	59.7	4643	14	US-10-072-621-2	Sequence 2, Appl
21	2436	59.7	4643	15	US-10-097-340-1	Sequence 1, Appl
22	2436	59.7	4643	15	US-10-007-926A-258	Sequence 258, App
23	2436	59.7	4646	17	US-10-641-643-1167	Sequence 1167, Ap
24	2436	59.7	4646	17	US-10-343-657-1	Sequence 1, Appl
25	2436	59.7	8630	9	US-09-306-417-2	Sequence 1, Appl
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28	2425	59.5	4788	9	US-09-866-866A-7	Sequence 7, Appl
29	2404.5	58.9	4189	9	US-09-866-866A-5	Sequence 5, Appl
30	2372	58.2	4254	9	US-09-917-800A-1424	Sequence 1424, Ap
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32	2372	58.2	4254	16	US-10-388-934-265	Sequence 265, App
33	2013.5	49.4	5010	9	US-09-917-800A-483	Sequence 483, App
34	1694	41.5	4175	9	US-09-749-340-3	Sequence 3, Appl
35	1694	41.5	4175	15	US-10-456-815-3	Sequence 3, Appl
36	1690.5	41.4	4002	9	US-09-758-828-1	Sequence 1, Appl
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38	1678.5	41.1	3512	9	US-09-749-340-7	Sequence 7, Appl
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40	1669.5	40.9	3861	9	US-09-938-842A-2237	Sequence 2237, Ap
41	1669.5	40.9	3861	11	US-09-938-842A-2237	Sequence 2237, Ap
42	1617	39.6	2698	9	US-09-749-340-5	Sequence 5, Appl
43	1617	39.6	2698	15	US-10-456-815-5	Sequence 5, Appl
44	1606	39.4	3921	16	US-10-280-238-848	Sequence 848, App
45	1586.5	38.9	2905	13	US-10-425-114-34865	Sequence 34865, A

ALIGNMENTS

RESULT 1
US-09-873-409-10
; Sequence 10, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; FILE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-409-10

Alignment Scores:
Pred. No.: 0
Score: 4079.00
Length: 2856
Matches: 812

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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Db 478 GTGGTTAGTCAGAGCGCTGTTTGTTCGGGACCAACCATCAGTAACAAATATCAAGATGGA 537

Qy 41 ArgAspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAsp 60
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Qy 81 SerGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIle 100
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Qy 101 LeuIleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAla 120
Db 718 CTGATTTTAGATGAGGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777

Qy 121 AlaLeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThr 140
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Qy 521 MetAlaIleGlyIleThrLeuValLeuAlaProGluTyrSerLysAlaLysSerGlyAla 540
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Qy 561 LysLysProAspThrCysGluGlyAsnLeuGluPheArgGluValSerPheTyrPro 580
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Db 2218 GTAGCATTTGTGGGAGACAGCGCTGTGGAAAGACACTTCTGTTCACTTCTGACAGACA 2277

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RESULT 2
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; Sequence 12, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 3177
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: No. US20020037522A1e
; LOCATION: (198)...(198)
; OTHER INFORMATION: n at position 198 represents any nucleotide (A, T, C or G)
US-09-873-409-12

Alignment Scores:
Pred. No.: 0 Length: 3177
Score: 4079.00 Matches: 812
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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DB 799 GTGGTTAGTCAAGAGCGCTGTTTGTTCGGGACCCACCATCAGTAACAATATCAAGTATGGA 858
QY 41 ArgAspAspValThrAspGluGlnMetGluArgAlaAlaArgGluAlaAsnAlaTyrAsp 60
DB 859 CGAGATGATGTGACTGATGAGAGATGGAGAGGCGAGGCGAAGGAGCAATTCGGTATGAT 918
QY 61 PheIleMetGluPheProAsnIysPheAsnThrLeuValGlyGlyAlaGlnMet 80

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QY 81 SerGlyGlyGlnIysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProIysIle 100
DB 979 AGTGGAGGCGAGAAACAGAGGATCGCAATGCTGCTGCTTTAGTTTCGAAACCCCAAGATT 1038
QY 101 IleuIleLeuAspGluAlaThrSerAlaLeuAspSerGluSerIysSerAlaValGlnAla 120
DB 1039 CTGATTTTATGATGAGGCTACGCTCTGCCCTGATTCAGAAAGCAAGTCAGCTGTTTCAAGCT 1098
QY 121 AlaLeuGluIysAlaSerIysGlyArgThrThrIleValValAlaHisArgLeuSerThr 140
DB 1099 GCACGTGAGAGGCGAGCAAAAGTTCGACTACATCGTGTAGGACACCCGACTTTCTACT 1158
QY 141 IleArgSerAlaAspLeuIleValThrLeuIysAspGlyMetLeuAlaGluIysGlyAla 160
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QY 201 LeuProteinHisSerValIysSerIleIysSerAspPheIleAspLysAlaGluGluSer 220
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QY 221 ThrGlnSerIysGluIleSerLeuProGluValSerLeuLeuIysIleLeuIysLeuAsn 240
DB 1399 ACCCAATCTAAAGAGATAAGTCTTCTCTGAAGTCTCTCTATTAAAAATTTTAAAGTTAAAC 1458
QY 241 LysProGluTyrProPheValValIleGlyThrLeuAlaSerValLeuAsnGlyThrVal 260
DB 1459 AAGCTTGAATGGCTTTTGTGGTCTCTGGGACATTTGGCTTCTTCTTAAATGGAACTGTT 1518
QY 261 HisProValPheSerIleIlePheAlaIysIleIleThrMetPheGlyAsnAsnAspLys 280
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QY 281 ThrThrIleIysHisAspAlaGluIleTyrSerMetIlePheValIleIleGlyValIle 300
DB 1579 ACCCATTTAAAGCATGATGTCAGAAATTTATTCATGATATTCGTCATTTTGGGTGTTATT 1638
QY 301 CysPheValSerTyrPheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThr 320
DB 1639 TGCTTTGTCAGTTATTTTCATCGAGGATTTTTCGGCAGAGCAGGCGGAAATTTTAACG 1698
QY 321 MetArgLeuArgHisLeuAlaPheIysAlaMetLeuTyrGlnAspIleAlaThrPheAsp 340
DB 1699 ATGAGATTAAAGACACTTGGCTTCAAGGCCATGTTATATCATCAGGATATTGCTGTTTGTAT 1758
QY 341 GluIysGluAsnSerThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIle 360
DB 1759 GAAAGGAAACACACAGGAGGCTTGACAAATATTTAGCCATAGATATAGCAAAAT 1818
QY 361 GlnGlyAlaThrGlySerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeu 380
DB 1819 CAAGGAGCAACAGGTTCCAGGATTTGGGCTTTAAACACAAAATGCAACTAATCATGAGACTT 1878
QY 381 SerValIleIleSerPheIleTyrGlyTyrMetThrPheLeuIleLeuSerIleAla 400
DB 1879 TCAGTTATCATTTCTCTTATATATGATGGAGATGACATTCCTTGATTTCTGAGTATTGCT 1938
QY 401 ProValLeuAlaValThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLys 420
DB 1939 CCAGTACTTCCGCGGACAGGAATGATTTGAAACCCGACCAATGACTGGATTTGCCAACAAA 1998
QY 421 AspIysGlnGluLeuLeuHisAlaGlyIysIleAlaThrGluAlaLeuGluAsnIleArg 440
DB 1999 GATAAGCAAGAACTTAAGCATGCTGGAAAGATAGCAACTGAAGCTTTGGAGATATACGT 2058

Qy 441 ThrIleValSerLeuThrArgGluLysAlaPheGluMetTyrGluGluMetLeuGln 460
Db 2059 ACTATAGTGTATTAACAAGGGAAGAAAGCCCTTCAGCAAAATGTATGAAGAGATGCTTCAG 2118
Qy 461 ThrGlnHisArgAsnThrSerLysLysAlaGlnIleileGlySerCysTyrAlaPheSer 480
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Qy 481 HisAlaPheIleTyrPheAlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGln 500
Db 2179 CATGCCCTTTATATTTGCTATGATGACAGAGGGTTTCGATTTGGAGCTATTTAAATCAA 2238
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Db 2239 GCTGGACGATATGACCCCGAGAGCGCANGTTCTATAGTTTTCATGCAATTCGATATGAGCT 2298
Qy 521 MetAlaIleGlyLysThrLeuValLeuAlaProGluTyrSerLysAlaLysSerGlyAla 540
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Qy 561 LysLysProAspThrCysGluGlyAsnLeuGluPheArgGluValSerPheTyrPro 580
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Qy 621 LeuTyrAspProValGlnGlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsn 640
Db 2599 CTTTATGACCCCGTGCAGGACAGTCTGTTGATGTTGTGGATGCAAAAGAAATTTGAAT 2658
Qy 641 ValGlnTrpLeuArgSerGlnIleAlaIleValProGlnGluProValLeuPheAsnCys 660
Db 2659 GTACAGTGGCTCCGTTCCCAATAGCAATCGTTCTCAAGAGCTGTGCTCTTCACTGC 2718
Qy 661 SerIleAlaGluAsnIleAlaTyrGlyAspAsnSerArgValValProLeuAspGluIle 680
Db 2719 AGCATTTGCTGAGAAACATCGCTATGTTGACACAGCCGTTGTGTCCTATGATGATC 2778
Qy 681 LysGluAlaAlaAsnAlaAlaAsnIleHisSerPheIleGluGlyLeuProGluLysTyr 700
Db 2779 AAAGAAGCCGCAATGCGAGCAAAATATCCATCTCTTTTATGAAGTCTCCCTGGAATATC 2838
Qy 701 AsnThrGlnValGlyLeuLysGlyValAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAla 720
Db 2839 AACACACAGTTGGCTGMAAGGAGACAGCTTTCTGGCGGCAGAAACAAAGACTAGCT 2898
Qy 721 IleAlaArgAlaLeuLeuGlnLysProLysIleLeuLeuLeuAspGluAlaThrSerAla 740
Db 2899 ATTCAAGGGCTCTCTCCAAAAACCCAAAAATTTTATTTGGATGAGGCACTTCAGCC 2958
Qy 741 LeuAspAsnAspSerGluLysValValGlnHisAlaLeuAspLysAlaAaThrGlyArg 760
Db 2959 CTCGATATGACATGAGAGGTGCTTCAGCATCCCTTCGATAAGCCAGGAGGAGG 3018
Qy 761 ThrCysLeuValValThrHisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValVal 780
Db 3019 ACATGCCCTAGTGGTCACTCACAGGCTCTCTGCAATTCAGAACGAGATTTGATAGTGGTT 3078
Qy 781 LeuHisAsnGlyLysIleLysGluGlnGlyThrHisGlnGluLeuLeuAaGsnArgAsp 800
Db 3079 CTGCACATGGAAGATTAAGAAACAGGAACCTCATTCAGAGCTCTCTGAGAAATCGAGAC 3138

Qy 801 IleTyrPheLysLeuValAsnAlaGlnSerValGln 812
Db 3139 ATATATTTTAAGTTTATGATGACATGCAGTCAGTCAGTCAG 3174
RESULT 3
US-09-873-409-14
: Sequence 14, Application US/09873409
: Patent No. US20020037522A1
: GENERAL INFORMATION:
: APPLICANT: Frank, Markus
: APPLICANT: Sayegh, Mohamed
: TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
: TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
: FILE REFERENCE: 81994/268611
: CURRENT APPLICATION NUMBER: US/09/873,409
: CURRENT FILING DATE: 2001-06-05
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 14
: LENGTH: 3621
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-873-409-14
Alignment Scores:
Pred. No.: 0 Length: 3621
Score: 4079.00 Matches: 812
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-873-409-2 (1-812) x US-09-873-409-14 (1-3621)
Qy 1 MetValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGly 20
Db 1183 ATGGTGGATGAGATGACATCAGAGCTTTAAATGTGGCATTATCGAGACCATATTGGA 1242
Qy 21 ValValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGly 40
Db 1243 GTGGTGTAGTCAAGAGCCCTGTTTGTTCGGGACCCACCATCAGTAAACAATATCAAGTATGA 1302
Qy 41 ArgAspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAsp 60
Db 1303 CGAGATGATGTGATGATGAGAGATGAGAGAGCAGCAGGAGGAGCAATCGGTATGAT 1362
Qy 61 PheIleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMet 80
Db 1363 TTTATCATGGAGTTTCTCTAATAAATTTAATACTATGTTGGTGGGAAAAAGGAGCTCAAAATG 1422
Qy 81 SerGlyGlyGlnLysGlnArgIleAlaIleAlaAlaLeuValArgAsnProLysIle 100
Db 1423 AGTGGGGGCGAAGACAGAGGATCGCATTTGCTCTGCTTAGTTTGAACCCCAAGATT 1482
Qy 101 LeuIleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAla 120
Db 1483 CTGATTTTATGATGAGGCTACGCTGCTGCTGGATTTCAGAAAGCAAGTCAGCTGTTCAAGCT 1542
Qy 121 AlaLeuLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThr 140
Db 1543 GCACCTGGAAGCGGAGGAGGAGGTCGAGTCAATTCGTTGGTGTAGCACCAGCATTTTCTACT 1602
Qy 141 IleArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGlyLysGlyAla 160
Db 1603 ATTCGAAGTCAGATTTGATTTGACCTTAAAGGATGGAATGCTGCGGAGAAAGGAGCA 1662
Qy 161 HisAlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGlnAspIle 180
Db 1663 CATGCTGAACTAATGCAAAACAGGCTCTATATTATTCTCTTGTGATGTCAGAGATATT 1722
Qy 181 LysLysAlaAspGluGlnMetGluSerMetThrTyrSerThrGluArgLysThrAsnSer 200
Db 1723 AAAAAAGCTGATGACAGATGAGTCAATGACATATTCTTACTGAAAGAAAGACCAACTCA 1782

201 LeuProLeuHisSerValLysSerIleLeuSerAspPheIleAspLysAlaGluGluSer 220
1783 CTTCCCTCTGCACTCTGTGAAGAGCATCAAGTCAAGTTCATTGACAAAGGCTGAGGAATCC 1842
221 ThrGlnSerLysGluIleSerLeuProGluValSerLeuLeuLysIleLeuLysLeuAsn 240
1843 ACCCAATCAAGAGATAAGTCTTCCTGAGTCTCTCTATTAATAAATTTTAAAGTTAAAC 1902
241 LysProGluTrpProPheValValLeuGlyThrLeuAlaSerValLeuAsnGlyThrVal 260
1903 AAGCCCTGAATGGCTTTTGTGGTCTTGGGACATGGCTTCTGTCTTAATAATGAACTGTT 1962
261 HisProValPheSerIleIlePheAlaLysIleIleThrMetPheGlyAsnAsnAspLys 280
1963 CATCCAGTATTTCCATCATCTTTGCCAAATAATTAACCATGTTTGGAAATAATGATAA 2022
281 ThrThrLeuLysHisAspAlaGluIleThrSerMetIlePheValIleLeuGlyValIle 300
2023 ACCACATTAAGCATGATGAGAAATTTATTTCCATGATATTCGTCAATTTTGGGTGTATT 2082
301 CysPheValSerThrPheValGlnGlyLeuPheThrGlyValAlaGlyGluIleLeuThr 320
2083 TGTCTTCTGATTTATTTCTGAGGATTTATTTTACGGCAGACGAGGGGAAATTTTACG 2142
321 MetArgLeuArgHisLeuAlaPheLysAlaMetLeuThrGlnAspIleAlaTrpPheAsp 340
2143 ATCAGATTAAGACACTTGGCCCTTCAAGCCATGTTATATCAGGATATTCCTGGTTGAT 2202
341 GluLysGluAsnSerThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIle 360
2203 GAAAGAAACAGCAGAGGCTTGACMACAATATTTAGCCATAGATATAGCAAAAT 2262
361 GlnGlyAlaThrGlySerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeu 380
2263 CAAGGAGCAACAGGTTCCAGGATTTGGCTTTAAACACAAATGCAACTAACATGGGACTT 2322
381 SerValIleLeuSerPheIleThrGlyTrpGluMetThrPheLeuIleLeuSerIleAla 400
2323 TCAGTTATCATATTTCCCTTATATGATGAGGAGATGACATTCCTGATTTCTGAGTATTGCT 2382
401 ProValLeuAlaValThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLys 420
2383 CCAGTACTTCCCTGACAGGAATGATTGAACCCGACGACATGATGATTTGCCAACAA 2442
421 AspLysGlnGluLeuLysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArg 440
2443 GATAAGCAGAGACTTAAGCATGCTGGAAGATAGCAACTGAAGCTTTGGAGAAATATACGT 2502
441 ThrIleValSerLeuThrArgGluLysAlaPheGluGlnMetThrGluGluMetLeuGln 460
2503 ACTATAGTGTCTTAACAGGGGAAAAGCCCTTCAGCAAAATGTATGAGAGATGCTTCAG 2562
461 ThrGlnHisArgAsnThrSerLysLysAlaGlnIleIleGlySerCysThrAlaPheSer 480
2563 ACTCAACACAGAAATACCTCGAAGAAAGCACAGATTAATTTGGAAGCTGTTATGCAATTCAG 2622
481 HisAlaPheIleThrPheAlaThrAlaAlaGlyPheArgPheGlyAlaThrLeuIleGln 500
2623 CATGCCCTTTATATTTTGCCTATGAGGAGGCTTTCGATTTGGAGCCCTATTTAATTCAA 2682
501 AlaGlyArgMetThrProGluGlyMetPheIleValPheThrAlaIleAlaThrGlyAla 520
2683 GCTGGAGCAATGATCCCCAGAGGCGCATGTTTCATAGTTTTTACTGCAATTCATATGGAGCT 2742
521 MetAlaIleGlyLysThrLeuValLeuAlaProGluThrSerLysAlaLysSerGlyAla 540
2743 ATGCCATCGGAAAAACGCTGCTTTGGCTCCTGAAATATTTCCAAAGCCAAATTCGGGGCT 2802
541 AlaHisLeuPheAlaLeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGly 560
2803 GCSCATCTGTTGCTTTGTTGGAAAGAAACCAATATATAGACAGCCGAGTCAAGAGGG 2862

561 LysLysProAspThrCysGluGluValAsnLeuGluPheArgGluValSerPhePheThrPro 580
2863 AAAAAGCCAGACACACATGTGAAGGGAATTTAGAGTTTCGAGAGTCTCTCTTCTATCCA 2922
581 CysArgProAspValPheIleLeuArgGlyLeuSerLeuSerIleGluArgGlyLysThr 600
2923 TGTCCGCCAGATGTTTTCATCCTCCGTGGCTTATCCCTCAGTATTGAGCGAAGAGACA 2982
601 ValAlaPheValGlySerSerGlyCysGlyLysSerThrSerValGlnLeuLeuGlnArg 620
2983 GTAGCATTTTGGGAGAGACGGCTGTGGGAAAGACATCTCTGTTCACTTCTGCAGAGA 3042
621 LeuThrAspProValGlnGlnValLeuPheAspGlyValAspAlaLysGlnLeuAsn 640
3043 CTTTATGACCCCGTCCCAAGCAAGTGTCTTGTATGTGTGGATGTCGAAAGATTTGAT 3102
641 ValGlnTrpLeuArgSerGlnIleAlaIleValProGlnGluProValLeuPheAsnCys 660
3103 GTACAGTGGCTCCGTTCCCAATAGCAATGCTTCTCAAGAGCCGTGTCTTCAACTGC 3162
661 SerIleAlaGluAsnIleAlaThrGlyAspAsnSerArgValValProLeuAspGluIle 680
3163 AGCATTTGCTGAGAACATCGCTATGTGACAAACCCGCTGTGTGTCCTATTAGATC 3222
681 LysGluAlaAlaAsnAlaAlaAsnIleHisSerPheIleGluGlyLeuProGluLysThr 700
3223 AAAGAAAGCCGCAATTCGAGCAAAATATCCATCTTTTATTGAGGTCTCCCTGAGAAATAC 3282
701 AsnThrGlnValGlyLysGlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAla 720
3283 AACACACAGTTGGACTGAAGGACACAGCTTTCTGGGCGCCAGAACAAAGACTAGCT 3342
721 IleAlaArgAlaLeuLeuGlnLysProLysIleLeuLeuLeuAspGluAlaThrSerAla 740
3343 ATTGCAAGGCTCTTCTCCAAAACCCCAAAATTTTATTGTTGGATGAGGCCACTTCAGCC 3402
741 LeuSerAsnAspSerGluLysValValGlnHisAlaLeuAspLysAlaArgThrGlyArg 760
3403 CTCGATATGACGTGAGAGTGGTTTCAGCATGCCCTTGATTAAGCCAGGACGGGAGG 3462
761 ThrCysLeuValValThrHisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValVal 780
3463 ACATGCCCTAGTGGTCACTCACAGGCTCTCTGCAATTCAGAAACGACAGATTTGATAGTGGT 3522
781 LeuHisAsnGlyLysIleGlyGluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAsp 800
3523 CTGCAATATGAGAAATTAAGAGAACAGAACTCATCAAGAGCTCTCTGAGAAATTCAGAC 3582
801 IleThrPheLysLeuValAsnAlaGlnSerValGln 812
3583 ATATATTTTAAAGTTAGTGAATGCACAGTCAGTGCAG 3618

RESULT 4

US-09-873-409-13
; Sequence 13, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; FILE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 3702
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: No. US20020037522A1e
; LOCATION: (723)...(723)

OTHER INFORMATION: n at position 723 represents any nucleotide (A, T, C or G)

US-09-873-409-13		US-09-873-409-13 (1-3702)	
Alignment Scores:			
Pred. No.:	0	Length:	3702
Score:	4079.00	Matches:	812
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0
US-09-873-409-2 (1-812) x US-09-873-409-13 (1-3702)			
Qy	1	MetValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGly	20
Db	1264	ARGGGATGGATGAGATGACATCAGAGCTTTAAATGTGGCGCATATTCGAGACCATATGGA	1323
Qy	21	ValValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGly	40
Db	1324	GTGGTTAGTCAAGAGCCGTGTTTGTGGGACCACCATCACTAACAATATCAAGTATGGA	1383
Qy	41	ArgAspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAsp	60
Db	1384	CGAGATGATGTACTGATCAAGAGATGGAGAGCGAGCGAGCGAAGCAAAATGCCGTATGAT	1443
Qy	61	PheIleMetGluPheProAsnIysPheAsnThrLeuValGlyGluLysGlyAlaGlnMet	80
Db	1444	TTTATCATGGAGTTTCTTAATAAATTTATACATTTGGTAGGGAAAAAGGAGCTCAATG	1503
Qy	81	SerGlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIle	100
Db	1504	AGTGAGGGCGAGAAACAGAGGATCCCAATTCGTGCTTGTAGTTTCGAAACCCCAAGATT	1563
Qy	101	LeuIleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAla	120
Db	1564	CTGATTTAGATGAGCTACGTCCTCCCTGGATTCAGAAAGCAAGTACGCTTTCAGCT	1623
Qy	121	AlaLeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThr	140
Db	1624	GCATCGAGAGCGGAGCAAGGTCGGACTCAATCGTGGTAGCACACCGACTTCTACT	1683
Qy	141	IleArgSerAlaAspIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAla	160
Db	1684	ATTCAAGTGGAGATTGATGTGACCTTAAGAGGAAATGCTCGCGGAGAAAGGAGCA	1743
Qy	161	HisAlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGlnAspIle	180
Db	1744	CATGCTGAACATAATGGCAAAACGAGGCTATATATTTCATCTGTGATGTCACAGGATATT	1803
Qy	181	LysLysAlaAspGluGlnMetGluSerMetThrTyrSerThrGluArgLysThrAsnSer	200
Db	1804	AAAAAAGCTGATGAACAGATGGAGTCAATGACATATTCTACTGAAGAAGAACCAACTCA	1863
Qy	201	LeuProLeuHisSerValLysSerIleLysSerAspPheIleAspLysAlaGluGluSer	220
Db	1864	CTTCCTCTGCATCTGTGAAGAGCATCAAGTCAGACTTCATTCAGCAAGGCTGAGGAATCC	1923
Qy	221	ThrGlnSerLysGluIleSerLeuProGluValSerLeuLeuLysIleLeuLysLeuAsn	240
Db	1924	ACCCCAATCTAAAGAGATAAGTCTTCGAAAGTCTCTCTATTAATAAATTTTAAAGTTAAAC	1983
Qy	241	LysProGluTyrProPheValValLeuGlyThrLeuAlaSerValLeuAsnGlyThrVal	260
Db	1984	ARGCCTGAATGGCCCTTTGTGTTCTGGGACATTTGGCTTCTCTTAATGGCACTGTT	2043
Qy	261	HisProValPheSerIlePheAlaLysIleIleThrMetPheGlyAsnAsnAspLys	280
Db	2044	CATCCAGATATTTTCCATCATCTTTGCAAAAATTTATAACCATCTTTTGGAAATTAATGATAA	2103
Qy	281	ThrThrLeuLysHisAspAlaGluIleTyrSerMetIlePheValIleLeuGlyValIle	300
Db	2104	ACCACATTAAAGCATGATCGAATAATTTATTTCATGATATTCTGTCATTTTGGGTGTTATT	2163
Qy	301	CysPheValSerTyrPheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThr	320
Db	2164	TGCTTTGTTCAGTTATTTTCATGCGAGGATTTATTTACGGCAGACGAGGGAATTTTAAAG	2223
Qy	321	MetArgLeuArgHisLeuAlaPheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAsp	340
Db	2224	ATGAGATTAAAGACACTTGGCTTCAAGGCCATGTTATATACAGGATTTGCTTGGTTGAT	2283
Qy	341	GluLysGluAsnSerThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIle	360
Db	2284	GAAGAAGAAACAGACAGGAGGCTTTGACACAATATTAGCCATAGATATAGCAAAAT	2343
Qy	361	GlnGlyValaThrGlySerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeu	380
Db	2344	CAAGAGACACAGGTTCCAGATGGCTTCTTAACACAAAATGCACACTACATGGGACTT	2403
Qy	381	SerValIleIleSerPheIleTyrGlyTyrGluMetThrPheLeuIleLeuSerIleAla	400
Db	2404	TCAGTTATCATTTTCTTTATATATGATGGAGATGACATTCCTGATTTCTGAGTATTGCT	2463
Qy	401	ProValIleAlaValThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLys	420
Db	2464	CCAGTACTTCCCGTGACAGGATGATTGAACCCGAGCAATGACTGGATTTGCCACRAA	2523
Qy	421	AspLysGlnGluLeuLysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArg	440
Db	2524	GATAAGCAAGAACTTAAGCATGCTGGAAGATAGCAACTGAAGCTTTGGAGAAATATACGT	2583
Qy	441	ThrIleValSerLeuThrArgGluLysAlaPheGluGlnMetTyrGluGluMetLeuGln	460
Db	2584	ACTATAGTGTCTATTAACAAGGAAAGCCCTCGAGCAATGTATGAAGAGATGCTTTCAG	2643
Qy	461	ThrGlnHisArgAsnThrSerLysLysAlaGlnIleIleGlySerCysTyrAlaPheSer	480
Db	2644	ACTCAACACAGAAATACCTCGAAGAAAGCACAGATTTATTGGAAGCTGTTATGCAATCAGC	2703
Qy	481	HisAlaPheIleTyrPheAlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGln	500
Db	2704	CATGCCCTTATATATTTTGCCTATGTCAGCAGGCTTTCGATTTGAGACCTTATTTAATTCAA	2763
Qy	501	AlaGlyArgMetThrProGluGlyMetPheIleValPheThrAlaIleAlaTyrGlyAla	520
Db	2764	GCTGGAGCAATGATCCCGAGGCGCATGTTCTATAGTTTCTTACTGCAATTCATATGAGCT	2823
Qy	521	MetAlaIleGlyLysThrLeuValLeuAlaProGluTyrSerLysLysLysSerGlyAla	540
Db	2824	ATGSCCATCGAAAAACGCTCGTTTGGCTCTCGAAATATTTCCAAAGCCAAATCGGGGCT	2883
Qy	541	AlaHisLeuPheAlaLeuLeuGluLysLysProAsnIleAspSerArgSerGlnGly	560
Db	2884	GCGCATCTGTTTGCCTTGTGGAAAGAAACCAATATAGACAGCCGCGAGTCAAGAAAGG	2943
Qy	561	LysLysProAspThrCysGluGlyAsnLeuGluPheArgGluValSerPhePheTyrPro	580
Db	2944	AAAAAGCCAGACATGTGAAGGGAAATTTAGAGTTTCGAGAGCTCTCTTTCTTCTATCCA	3003
Qy	581	CysArgProAspValPheIleLeuArgGlyLeuSerLeuSerIleGluArgGlyLysThr	600
Db	3004	TGTGCCCCAGATGTTTTCATCTCCCGTGGCTTATCCCTCAGTATGAGCGGAGAGACA	3063
Qy	601	ValAlaPheValGlySerSerGlyCysGlyLysSerThrSerValGlnLeuLeuArg	620
Db	3064	GTAGCATTTGTGGGAGCAGCGCTGTGGGAAAAAGCACTTCTGTTCAACTTCTGCAGAGA	3123
Qy	621	LeuTyrAspProValGlnGlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsn	640
Db	3124	CTTTATGACCCCGTGAAGGACCAAGTCTGTTGATGGTGTGGATGCAAAAGAAATTTGAT	3183
Qy	641	ValGlnTyrLeuArgSerGlnIleAlaIleValProGlnGluProValLeuPheAsnCys	660
Db	3184	GTACAGTGGCTCGCTTCCCAATAGCAATCGTTCCTCAAGAGCTGTGCTCTTCAACTGC	3243
Qy	661	SerIleAlaGluAsnIleAlaTyrGlyAspAsnSerArgValValProLeuAspGluIle	680

Qy 281 ThrThrLeuLysHisAspAlaGluIleTyrSerMetIlePheValIleLeuGlyValIle 300
Db 2179 ACCACATTTAAAGCATGATGACAGAAATTTATTCATGATATTCGTCAATTTGGGTGTTATT 2238
Qy 301 CysPheValSerTyrPheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThr 320
Db 2239 TGCCTTGGCAGTTTATTCATG----- 2259
Qy 321 MetArgLeuArgHisLeuAlaPheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAsp 340
Db 2260 -----CAGGATATTGCGTGGTTGAT 2280
Qy 341 GlnLysGlnSerThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIle 360
Db 2281 GAAAGGAAACACACACAGGAGGCTTGACAAATATTAGCCATAGATATAGCACAAATT 2340
Qy 361 GlnGlyAlaThrGlySerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeu 380
Db 2341 CAAGGAGCAACAGGTTCCAGGATTGGCGTCTTAACACAAAAATGCACTACATCGGACTT 2400
Qy 381 SerValIleIleSerPheIleTyrGlyTyrGluMetThrPheIleIleLeuSerIleAla 400
Db 2401 TCAGTTATCATTTCTCTTATATATGAGTGGAGATGATCATTCCTGATTTCTGAGTATTGCT 2460
Qy 401 ProValLeuAlaValThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLys 420
Db 2461 CCAGTACTTGGCGTGACAGGATGATTTGAACCCGACGATGACTGGATTTGCCACAAA 2520
Qy 421 AspLysGlnGluLeuLysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArg 440
Db 2521 GATAAGCAAGAACTTAAGCATGCTGGAAGATAGCAACTGAAGCTTTGGAGAAATATACGT 2580
Qy 441 ThrIleValSerLeuThrArgGluLysAlaPheGluGlnMetTyrGluGluMetLeuGln 460
Db 2581 ACTATAGTGTCTATTAAACAGGGAANAAGCCCTTCAGCAATGATATGAAGAGATGCTTCAG 2640
Qy 461 ThrGlnHisArgAsnThrSerLysLysAlaGlnIleIleLeuGlySerCysTyrAlaPheSer 480
Db 2641 ACTCAACACAGAAATACCTCGAAGAAAGCACAGATTTATTTGAAGCTGCTTATGCAATTCAGC 2700
Qy 481 HisAlaPheIleTyrPheAlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGln 500
Db 2701 CATGCCCTTATATTGCTATGCGCGAGGTTTCGATTTGGAGCTTATTAATTCAA 2760
Qy 501 AlaGlyArgMetThrProGluGlyMetPheIleValPheThrAlaIleAlaTyrGlyAla 520
Db 2761 GCTGGAGCAATGATGCCAGAGGCGATGTTCATAGTTTACTGCAATTTGCATATGGAGCT 2820
Qy 521 MetAlaIleGlyLysThrLeuValLeuAlaProGluTyrSerLysAlaLysSerGlyAla 540
Db 2821 ATGCCCATCGAGAAACGCTCGTFTTGGCTCCTCGAATATTCCAAAGCCAAATCGGCGCT 2880
Qy 541 AlaHisLeuPheAlaLeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGly 560
Db 2881 GCGCATCTGTTTGGCTTTGGAAAGAAACCAAAATATACACAGCCGCACTCAAGAGGG 2940
Qy 561 LysLysProAspThrCysGluGlyAsnLeuGluPheArgGluValSerPhePheTyrPro 580
Db 2941 AAAAGGCGACACATGTGAAGGAAATTTAGAGTTTCGAAAGTCTCTTTCTCTATCCA 3000
Qy 581 CysArgProAspValPheIleLeuArgGlyLeuSerLeuSerIleGluArgGlyLysThr 600
Db 3001 TGTGCCCCAGATGTTTTCATCTCTCGTGGCTTATCCTCTAGTATTGGCGAGGAAAGACA 3060
Qy 601 ValAlaPheValGlySerSerGlyCysGlyLysSerThrSerValGlnLeuLeuGlnArg 620
Db 3061 GTAGCAATTTGGGGAGCAGCGGCTGTGGGAAAGCACTTCTGTTCAACTTCTGCAGAGA 3120
Qy 621 LeuTyrAspProValGlnGlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsn 640
Db 3121 CTTTATGACCCCGTCAGGACAGTGTCTGTTGATGGTGGATGCAAAAGAAATTTGAAT 3180
Qy 641 ValGlnTrpLeuArgSerGlnIleAlaIleValProGlnGluProValLeuPheAsnCys 660

Db 3181 GTACAGTGGCTCGTTCCTCCAAATAGCAATCGTTCCTCAAGAGCCTGTGCTCTTCAACTGC 3240
Qy 661 SerIleAlaGluAsnIleAlaTyrGlyAspAsnSerArgValValProLeuAspGluIle 680
Db 3241 AGCATTTGCTGAGAACATCGCCTATGATGACACAGCCGTGTGTGCCATTAGATGAGATC 3300
Qy 681 LysGluAlaAlaAsnAlaAlaAsnIleHisSerPheIleGluGlyLeuProGluLysTyr 700
Db 3301 AAAGAGCGCAAAATCGACAAATATCCATTTCTTTATTGAAAGTCTCCCTCGAGAAATAC 3360
Qy 701 AsnThrGlnValGlyLeuLysGlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAla 720
Db 3361 AACACAAAGTTGGATCGAAGGAGCACAGCTTTCTGGCGGCCAGAAACAAGACTAGCT 3420
Qy 721 IleAlaArgAlaLeuLeuGlnLysProLysIleLeuLeuLeuAspGluAlaThrSerAla 740
Db 3421 ATTGCAAGGCTCTTCTCCAAAACCCAAAATTTTATTGTTGATCGAGCCACTTCAGCC 3480
Qy 741 LeuAspAsnAspSerCysLysValValGlnHisAlaLeuAspLysIleArgThrGlyArg 760
Db 3481 CTCGATAATGACAGTGAAGGTGGTTTCAGCATGCCCTTTGATAAAGCCAGGCGGGAAGG 3540
Qy 761 ThrCysLeuValValThrHisArgSerAlaIleGlnAsnAlaAspLeuIleValVal 780
Db 3541 ACATGCTTAGTGGTCACTCACAGGCTCTCTGCAATTCAGACGCAATTTGATGTTGTT 3600
Qy 781 LeuHisAsnGlyLysIleLysGluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAsp 800
Db 3601 CTGCAAAATGGAAGATAAAGCAAGGAATCTCATCAAGAGCTCTCTGAGAAATCGAGAC 3660
Qy 801 IleTyrPheLysLeuValAsnAlaGlnSerValGln 812
Db 3661 ATATATTTAAGTTAGTGAATCCACAGTCAGTCAG 3696

RESULT 6

US-09-873-409-9
; Sequence 9, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; FILE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-409-9

Alignment Scores:

Pred. No.: 0 Length: 2066
Score: 3456.00 Matches: 687
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.73% Indels: 0
DB: 9 Gaps: 0

US-09-873-409-2 (1-812) x US-09-873-409-9 (1-2066)

Qy 126 SerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIleArgSerAlaAsp 145
Db 3 ACCAAAGGTCCGACTACAAATCGTGTAGCACACCCAGCTTTCTACTATTTCGAAGTGCAGAT 62
Qy 146 LeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyValHisAlaGluMet 165
Db 63 TTGATTGTGACCTTAAAGATGGAATGCTGGCGGAGAAAGGAGACATGCTGAACATAATG 122

166 Qy AlalysArgGlyLeuTyrThrSerLeuValMetSerGlnAspIleLysLysAlaAspGlu 185
 123 Db GCAAAACGAGGCTATATTATTCATCTGTGATGTCACAGGATATTAATAAAGCTGATGA 182
 186 Qy GlnMetGluSerMetThrTyrSerThrGluArgLysThrAsnSerLeuProLeuHisSer 205
 183 Db CAGATGGAGTCAATGACATATTTCTACTGAAAGAAAGACCAACTCCTCTCTGCACTCT 242
 206 Qy ValLysSerIleLysSerAspPheIleAspLysAlaGluSerThrGlnSerLysGlu 225
 243 Db GTGAAGAGCATCAAGTTCAGACTTCATTGACAAAGGCTGAGGAATCCACCCCAATTAAGAG 302
 226 Qy IleSerLeuProGluValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTyrPro 245
 303 Db ATAAGTCTCTCTGAGGCTCTCTATTAATAAATTTAAAGATTAAACAAGCCCTGAATGGCCT 362
 246 Qy PheValValLeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSer 265
 363 Db TTGTGGTCTGCGGACATTTGGCTCTCTTAAATGGAACTGTTCAATCAGTATTTTCC 422
 266 Qy IleIlePheAlaLysIleIleThrMetPheGlyAsnAsnAspLysThrThrLeuLysHis 285
 423 Db ATCATCTTTGCAAAATTAATAACCATCTTTGGAAATTAATGATAAACACCATTAAGCAT 482
 286 Qy AspAlaGluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyr 305
 483 Db GATCAGAAATTTATTCATGATATTCATATTTGGTGTATTTCTTGTTCAGTTAT 542
 306 Qy PheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHis 325
 543 Db TTCATGCGAGGATTTATTTACGGCAGACGAGGGGAAATTTTAACGATGAGATTAAAGAC 602
 326 Qy LeuAlaPheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAspGluLysGluAsnSer 345
 603 Db TTGGCCCTCAAGCCATGTTATATTCAGGATATTCCTGGTGTGATGAAAGGAAACAGC 662
 346 Qy ThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGly 365
 663 Db ACAGAGGCTTGACACAAATATAGCCATAGATATAGCAAAATTCAGGAGCAACAGGT 722
 366 Qy SerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSer 385
 723 Db TCCAGGATGGCGTCTTAACACAAATAGCAACTAACATGGGACTTTTCAGTTATCATTTCC 782
 386 Qy PheIleTyrGlyTyrGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaVal 405
 783 Db TTTATATAGATGGGAGATGACATTCCTGATTTCTGATTTCTGAGATTTGCTCCAGTACTTCCGCTG 842
 406 Qy ThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeu 425
 843 Db ACAGGAATGATTGAACCGCAGCAATGACTGATTTGCCAACAAAGATAAGCAAGAATCT 902
 426 Qy LysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeu 445
 903 Db AAGCATGCTGGAAGATAGCAACTGAAGCTTTGAGAAATATACGTACTATAGTGTCAATTA 962
 446 Qy ThrArgGluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsn 465
 963 Db ACAAGGGAAGAGCTTCGAGCAATATGATGAGAGATGCTTCAGACTCAACACAGAAAT 1022
 466 Qy ThrSerLysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyr 485
 1023 Db ACCTCGAAGAAAGCACAGATTTATTTGAGAGCTGTTATGCAATTCAGCCATGCTTTATATAT 1082
 486 Qy PheAlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThr 505
 1083 Db TTTGCCCTATGACGAGGCTTCGATTTGGAGCTTATTTAATTCAGCTGAGCGATGACC 1142
 506 Qy ProGluGlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLys 525
 1143 Db CCAGAGGCGCATGTTCAATAGTTTACTGCAATTCATATGAGCTATGGAGCTATGGCAATCGGAAA 1202
 526 Qy ThrLeuValLeuAlaProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAla 545

1203 Db ACCTCGTITTTGGCTCTCTGAAATATTCCAAAGCCAAATCGGGGCTCGCATCTGTTTGGC 1262
 546 Qy LeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThr 565
 1263 Db TTGTTGGAAAGAAACCAATATAGACGCCGAGTCAAGAAAGGGAAGAAAGCCAGACACA 1322
 566 Qy CysGluGlyAsnLeuGluPheArgGluValSerPhePheTyrProCysArgProAspVal 585
 1323 Db TGTGAAGGGAATTTAGAGTTTCGAGAAATCTCTTCTCTCTATCCATGTGCGCCAGATGTT 1382
 586 Qy PheIleLeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGly 605
 1383 Db TTCATCTCTCGTGGCTTATCCCTCAGTATTGAGCGAGGAAGACAGTATTCATTTGGGG 1442
 606 Qy SerSerGlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProVal 625
 1443 Db ACAGCGGCTGTGGGAAAGACATCTCTGTTCAACTTCGACAGAGCTTTATGACCCCGTG 1502
 626 Qy GlnGlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnThrLeuArg 645
 1503 Db CAAGGACAAAGTCTGTTTGTATGTTGGATGCAAAAGAAATTTGAATGACAGTGGCTCCGT 1562
 646 Qy SerGlnIleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsn 665
 1563 Db TCCCAATAGCAATCTGTTCTCAAGAGCCTGTGCTCTTCACTGACAGCATTCGTGAGAAC 1622
 666 Qy IleAlaTyrGlyAspAsnSerArgValValProLeuAspGluIleLysGluAlaAlaAsn 685
 1623 Db ATGCCCTATGTGACAAACAGCGCTGTGTGTCCTCCTAGATGAGATCAAGAAAGCCGCAAT 1682
 686 Qy AlaAlaAsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGly 705
 1683 Db GCAGCAATATTCATCTCTTTATTTGAGGTCTCCCTGAGAAATACACACACAGTTGGA 1742
 706 Qy LeuLysGlyValAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeu 725
 1743 Db CTGAAAGGAGCAGCATCTTCTGGCGCCAGAAACAAAGACTAGCTATTTCAGGGCTCTT 1802
 726 Qy LeuGlnLysProLysIleLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSer 745
 1803 Db CTCCAAAACCCCAAAATTTTATTTGTTGATGAGGCCACTTCAGCCCTCCGATATGACAGT 1862
 746 Qy GluLysValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValVal 765
 1863 Db GAGAAGTGGTTCAGCATGCCCTTGATAAGCCAGGAGGAGGAGGACATGCCCTAGTGGTC 1922
 766 Qy ThrHisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLys 785
 1923 Db ACTCAGAGCTCTCTCAATTCAGAACGAGATTTGATAGTGTCTTCGACCAATGGAAG 1982
 786 Qy IleLysGluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeu 805
 1983 Db ATAAAGGAACNAGAACTCATCAGAGCTCTCGAGAAATCGAGACATATATTTTAAGTTA 2042
 806 Qy ValAsnAlaGlnSerValGln 812
 2043 Db GTGAATGCACAGTCACTGCGAG 2063

RESULT 7

US-10-092-900A-303
 ; Sequence 303, Application US/10092900A
 ; Publication No. US20040043382A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Padigar, Muraidhara
 ; APPLICANT: Spitek, Kimberly A.
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Taupier Jr., Raymond J.
 ; APPLICANT: Pena, Carol E.A.
 ; APPLICANT: Li, Li
 ; APPLICANT: Zerkhusen, Bryan D.
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Ji, Weizhen

```

1  APPLICANT: Gorman, Linda
2  APPLICANT: Miller, Charles E.
3  APPLICANT: Kekuda, Ramesh
4  APPLICANT: Patturajan, Meera
5  APPLICANT: Gangolli, Bsha A.
6  APPLICANT: Vernet, Corine A.M.
7  APPLICANT: Guo, Xiaojia Sasha T.
8  APPLICANT: Tchernev, Velizar T.
9  APPLICANT: Fernandes, Elma R.
10 APPLICANT: Casman, Stacie J.
11 APPLICANT: Malyankar, Uriel M.
12 APPLICANT: Gerlach, Valerie
13 APPLICANT: Liu Yi
14 APPLICANT: Anderson, David W.
15 APPLICANT: Spaderna, Steven K.
16 APPLICANT: Catterton, Elina
17 APPLICANT: Leite, Mario W.
18 APPLICANT: Zhong, Kaihong
19 APPLICANT: Alsobrook, John P.
20 APPLICANT: Lepley, Denise M.
21 APPLICANT: Rieger, Daniel K.
22 APPLICANT: Burgess, Catherine E.
23 APPLICANT: TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
24 FILE REFERENCE: 21402-290C
25 CURRENT APPLICATION NUMBER: US/10/092,900A
26 CURRENT FILING DATE: 2002-03-07
27 PRIOR APPLICATION NUMBER: USSN 60/274,322
28 PRIOR FILING DATE: 2001-03-08
29 PRIOR APPLICATION NUMBER: USSN 60/283,675
30 PRIOR FILING DATE: 2001-04-13
31 PRIOR APPLICATION NUMBER: USSN 60/338,092
32 PRIOR FILING DATE: 2001-12-03
33 PRIOR APPLICATION NUMBER: USSN 60/274,281
34 PRIOR FILING DATE: 2001-03-08
35 PRIOR APPLICATION NUMBER: USSN 60/274,191
36 PRIOR FILING DATE: 2001-03-08
37 PRIOR APPLICATION NUMBER: USSN 60/325,681
38 PRIOR FILING DATE: 2001-09-27
39 PRIOR APPLICATION NUMBER: USSN 60/304,354
40 PRIOR FILING DATE: 2001-07-10
41 PRIOR APPLICATION NUMBER: USSN 60/279,995
42 PRIOR FILING DATE: 2001-03-30
43 PRIOR APPLICATION NUMBER: USSN 60/294,899
44 PRIOR FILING DATE: 2001-05-31
45 PRIOR APPLICATION NUMBER: USSN 60/287,424
46 PRIOR FILING DATE: 2001-04-30
47 Remaining prior application data removed - See File Wrapper or PALM.
48 NUMBER OF SEQ ID NOS: 768
49 SEQ ID NO 303
50 LENGTH: 4091
51 TYPE: DNA
52 ORGANISM: Homo sapiens
53 FEATURE:
54 NAME/KEY: CDS
55 LOCATION: (16)..(4078)
56 US-10-092-900A-303
57
58 Alignment Scores:
59 Pred. No.: 7,72e-305 Length: 4091
60 Score: 3168.50 Matches: 677
61 Percent Similarity: 80.16% Conservative: 30
62 Best Local Similarity: 76.76% Mismatches: 62
63 Query Match: 17.68% Indels: 113
64 DB: 13 Gaps: 14
65
66 US-09-873-409-2 (1-812) x US-10-092-900A-303 (1-4091)
67
68 QY 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
69
70 DDB 1378 GTGGATGGTGTGATGCAAAAGAAATGAAATGATACAGTGGCTCGTCCCAAAATAGCAATC 1437
71
72 QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41

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QY 338 TrpPheAspGluLysGlnSerThrGlyLeuThrThrIleLeuAlaIleAspIle 357
DB 2461 TGGTTTGTATGAAGGAAACACACACAGAGGCTTGACACAAATATTAGCCATAGATATA 2520
QY 358 AlaGlnIleGlnGlyAlaThrGlySerArgIleGlyValLeuThrGlnAsnAlaThrAsn 377
DB 2521 GCACAAATTCAGAGGACACAGGCTTCAGGATTGGGGCTTTAACACACAAATGCACTAAC 2580
QY 378 MetGluLeuSerValIleIleSerPheIleTyrGlyTyrPheMetThrPheLeuIleLeu 397
DB 2581 ATGGGACTTTCAGTTATCATCTTCCTTTATATATGGATGGGAGATGACATTCCTGATCTG 2640
QY 398 SerIleAlaProValLeuAlaValThrGlyMetIleGluThrAlaAlaMetThrGlyPhe 417
DB 2641 AGTATTGCTCCAGTACTTGGCGTGACAGGAATGATTGAAACCGACCAATGACTGGATT 2700
QY 418 AlaAsnIysAspLysGlnGluLeuLysHisAlaGly-----LysIleAlaThrGluAla 435
DB 2701 GCCAAACAAGATAGCAAGAACTTAAGCATGCTGGAAAGGTAAGATAGCAACTGAAGCT 2760
QY 436 LeuGluAsnIleArgThrIleValSerLeuThrArgGluLysAlaPheGluGlnMetTyr 455
DB 2761 TTGGAGATATAGCTACTATAGTCTCATTAACACAGGGAAGAACCTTCGACGAAATGTAT 2820
QY 456 GluGluMetLeuGlnThrGlnHis----ArgAsnThrSerLysLysAlaGlnIleIleGly 474
DB 2821 GAAGAGATGCTTCAGACTCAACACAGAGAAATACCTCGAAGAAAGACAGATTATTGGA 2880
QY 475 SerCysTyrAlaPheSerHisAlaPheIleTyrPheAlaTyrAlaAlaGlyPheArgPhe 494
DB 2881 AGCTGTAATGCAATGACCATGCGCTTATATATTTCCTATGCGCAGGGTTTCGATT 2940
QY 495 GlyAlaTyrIleLeuGlnAlaGlyArgMetThrProGluGlyMetPhe---IleValPhe 513
DB 2941 GGAGCGCTATTAAATCAAGCTGACGAATGTCAATGCTTATCTTTTCATAGAGTTTT 3000
QY 514 ThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeuValIleAlaProGluTyr 533
DB 3001 ACTGCAATTCATATGAGCTATGGCCATCGGAAACGCTGTTTGGCTCTCTGAAATAT 3060
QY 534 SerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeuGluLysLysProAsnIle 553
DB 3061 TCCAAAGCCAAATCGGGGCTGGCATCTGTTGCTTGTGGAAAGAAACCAATATA 3120
QY 554 AspSerArgSerGlnGluGlyLysLysPro-----AspThrCysGluGlyAsnLeu 570
DB 3121 GACAGCGCAGTCAAGAAGGGAAGAAAGCCACTTTTCACAGGACACATGTGAAGGAATTTA 3180
QY 571 GluPheArgGluValSerPhePheTyrProCysArgProAspValPheIleLeuArgGly 590
DB 3181 GAGTTTCGAGAGTCTCTTCTTCTATCATGTGCGCCAGATGTTTCACTCTCCGTGTC 3240
QY 591 LeuSerLeuSerIleGluArgGlyLysThrValAlaPheValIleSerSerGlyCysGly 610
DB 3241 TTATCCCTCAGTATTGAGCGAGAAAGACAGTAGCATTTGTGGGAGCAGCGCTGTGGG 3300
QY 611 LysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGlyGlnValLeu 630
DB 3301 AAAAGCATTCTGTTCAACTTCCTGCGAGACTTTATGACCCCGTGCAGGACAAACAGCTG 3360
QY 631 PheAspGlyValAspAlaLysGluLeuAsnValGlnTyrPheArgSerGlnIleAlaIle 650
DB 3361 TTGTATGGTGTGATCAAAAGAAATGTAATGTACAGTGGCTCGTTCCTCCCAATAGCAATC 3420
QY 651 ValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAlaTyrGlyAsp 670
DB 3421 GTTCCTCAAGAGCGCTGCTCTCTTCAACTCAGCAGCATTTGCTGAGAACATCCCTATGCTGAC 3480
QY 671 AsnSerArgValValProLeuAspGluIleLysGluAlaAlaAsnAlaAlaAsnIleHis 690
DB 3481 AACAGCGCTGTGTTGCATTAGTGTAGATCAAGAGCGCGAAATGCAACCAATATCCAT 3540

QY 691 SerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLysGlyAlaGln 710
DB 3541 TCTTTTATTGAGGCTCTCCCT---AAATACACACACAAAGTTGGACTGAAGAGACACAG 3597
QY 711 LeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGlnLysProLys 730
DB 3598 CTTTCTGGCGGCAGAAACAAAGACTAGCTATTGCAAGGGCTCTTCTCCAAAACCCCAA 3657
QY 731 IleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLys-----Val 748
DB 3658 ATTATTATTGTTGGATGAGCCACTTCAGCCCTTCGATAATAGCAGTGAGAGGTACAGGTG 3717
QY 749 ValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHisArg 768
DB 3718 GTTCAGCATGCCCTTTGATAAGCCAGGAGGAGGACATGCTAGTGTCTACTCACAGG 3777
QY 769 LeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLysGlu 788
DB 3778 CTCTCTGCAATTTCAGACGCGAGATTGTAGTGGTCTTCACAAATGGAAAGATAAGGAA 3837
QY 789 GlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsnAla 808
DB 3838 CAAGGAACTCATCAGAGCTCTCTGGAATCGAGACATATATTTTAAGTTAGTGAATGCA 3897
QY 809 GlnSer 810
DB 3898 CAGTCA 3903

RESULT 8
US-10-363-112-48
; Sequence 48, Application US/10363112
; Publication No. US20040091964A1
; GENERAL INFORMATION:
; APPLICANT: THE AUSTRALIAN NATIONAL UNIVERSITY
; APPLICANT: HARRIS, MATTHEW
; TITLE OF INVENTION: MODIFIED PROTEINS, ISOLATED NOVEL PEPTIDES, AND USES THEREOF
; FILE REFERENCE: 007643-0302189
; CURRENT APPLICATION NUMBER: US/10/363,112
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/AU01/01093
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,663
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 3825
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3825)
; US-10-363-112-48

Alignment Scores:
Pred. No.: 7,65e-235 Length: 3825
Score: 2465.50 Matches: 478
Percent Similarity: 76.46% Conservative: 149
Best Local Similarity: 58.29% Mismatches: 182
Query Match: 60.44% Indels: 11
DB: 17 Gaps: 3

US-09-873-409-2 (1-812) x US-10-363-112-48 (1-3825)

QY 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
DB 1363 ATTGATGGCGAGGATATTAGGAACCTTTAATGTAACACTATCTCGAGGGAATCATTTGGTGG 1422
QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
DB 1423 GTGAGTCAGGAGCGGTGCTGTTTTCACCAACATGCTGGAATATTTTGTGTGGCCGT 1482

	DB	2563	CAAGTTAAACCCCTATTGCTATTAGCAGTGTTC	CAATATTGCTGTCAGGAATTGTTGAA	2622
	QY	411	ThralAalMetThrGlyPheAlaAsnLysAspLysGlnGlutLeuLysHISalaGlyLys	430	
	DB	2623	ATGAAATTCTGGCTCGAAATGCCAAAGAGATAAAAAAGAACTGGGAAGCTGCTGGAAA	2692	
	QY	431	IleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArgGluLysAla	450	
	DB	2683	ATTGCACAGAGCGCAATGAAAATATTAGACAGTGTGTGCTTTTGACCCAGGAAGAAAA	2742	
	QY	451	PheGluGlnMetTyrgluGluMetLeuGlnThrGlnHisArgAsnThrSerLysLysAla	470	
	DB	2743	TTTGAAATCAATGATGTTGAAAAATTGTATGGACCTTACAGGAATCTGTGCAGAAGCCA	2802	
	QY	471	GlnIleileGlySerCysTyralaPheSerHisAlaPheIleTyrbheAlatyrAlaAla	490	
	DB	2803	CACATCTATGGAATTACTTTTATCTCTCACAGCATTTATGTATTTTCTCTATGCCGGT	2862	
	QY	491	GlyPheArgPheClAlatyrLeuIleGlnAlaGlyArgMetThrProGluGlyMetPhe	510	
	DB	2863	TGTTTTGATTTGGTGCAATATCTCATGTGAATGGACATATGGCTTCAGAGATGTTATT	2922	
	QY	511	IleValPheThrAlaIleAlatyryGlyAlaMetAlaIleGlyLysThrLeuValLeuAla	530	
	DB	2923	CTGGTGTTTTCTGCAATTGTAATTGGTGCAATGGCTCTAGGACATGCCAGTTTCATTTGCT	2982	
	QY	531	ProGluTyrrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuGluLysLys	550	
	DB	2983	CAGACTATGCTAAAGCTTAAGCTGCTCGAGGCCACTTAITTCATGCTGTTTGAAGACA	3042	
	QY	551	ProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGluGlyAsnLeu	570	
	DB	3043	CCTCTGATTTGACAGCTACAGTGAAGAGGGCTGAAGCTTGATAAAATTGAAGGAATATA	3102	
	QY	571	GluPheArgGluValSerPhePheTyrrProCysArgProaspValPheIleLeuArgGly	590	
	DB	3103	ACATTTAAATGAAGTCGTGTCAACTATCCACC CGGAGCAAACGTGCCAGTTCCTCAGGGG	3162	
	QY	591	LeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSerGlyCysGly	610	
	DB	3163	CTGAGCCTGGAGGTGAAGAAAGGCCAGACACATAGCCCTGCTGGGCGACAGTGCCTGGG	3222	
	QY	611	LysSerThrServValGlnLeuLeuGlnArgLeuTyrrAspProValGlnGlyGlnValLeu	630	
	DB	3223	AAGAGCACGGTGTGCAGCTCTGTGAGCGGTTCACGACCCCTTGGCGGGGACAGTGCCT	3282	
	QY	631	PheAspGlyValAspAlaLysGluLeuAsnValGlnTrpLeuArgSerGlnIleAlaIle	650	
	DB	3283	CTCGATGGTTCAGAACCAAGAAACTCAATGTCAGTGGCTCAGAGCTCACTCGGAATC	3342	
	QY	651	ValProGlnIleProValLeuPheAsnCysSerIleAlaGluAsnIleAlatyrrGlyAsp	670	
	DB	3343	GTGCTCTCAGAGCGCTATCTTAITTGACTGCAGCATTTGCCAGAAATATTGCTCTATGGAGAC	3402	
	QY	671	AnnSerArgValValProLeuAspGluIleLysGluAlaAlaAsnAlaAlaAsnIleHis	690	
	DB	3403	AACAGCCGGGTGTATCAGAGATGAATTTGTGAGTGCAGCCAAAGCTGCACATACAT	3462	
	QY	691	SerPheIleGluGlyLeuProGluLysTyrrAsnThrGlnValGlyLeuLysGlyValGln	710	
	DB	3463	CCTTTTCATCGACAGCTTACCCCAACAATATGAAACAAGAGTGGGAGATAAGGGGACTCAG	3522	
	QY	711	LeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGlnLysProLys	730	
	DB	3523	CPCTCAGGAGGTCAAAAAAGAGGATTTGCTATTGCCCCGAGCCCTCATCAGCAACCTCCA	3582	
	QY	731	IleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLysValValcIn	750	
	DB	3583	ATCCTCTGTTGGATCAAGCTACATCAGCTCTGGATACTGAAAGTGAAGGTTGTCCAA	3642	
	QY	751	HISAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHisArgLeuSer	770	

Db	3643	GAAGCCCTGGACAAAGCCAGAGAAAGCCGCACTCGCATCTGTGATCTCTACACGCTCTGCC	3702
Qy	771	AlaIleGlnAsnAlaAspLeuIleValLeuHisAsnGlyIysLeIysGluGlnGly	790
Db	3703	ACCATCCAGAAATGCAGACTTAATAGTGTGTTTCAGAAATCGGAGAGTCAAGGAGCATGCC	3762
Qy	791	ThrHisGlnGluLeuLeuArgAsnArgAspIlePyrPhenIysLeuValAsnAlaGlnSer	810
Db	3763	ACGCATCAGCAGCTGCTGGCACAAAGAGCATTAATTTTCAATGGTCACTGTCACAGCT	3822

RESULT 9

```

US-09-880-107-2299
; Sequence 2299, Application US/09880107
; Patent NO. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Dargi T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44321-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2299
; LENGTH: 3924
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M2
US-09-880-107-2299

```

Alignment Scores:		
Pred. No.:	7,956-235	Length:
Score:	2465.50	Matches:
Percent Similarity:	76.46%	Conservative:
Best Local Similarity:	56.29%	Mismatches:
Query Match:	60.44%	Indels:
DB:	9	Gaps:
		3
		3324

US-09-873-409-2 (1-812) X US-09-880-107-2299 (1-3924)

Qy	2	VaaaspGluAsnAspIleAargAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal	21
Db	1395	AITGGATGGGCAGGATATTAGCAACTTTAACTGTAAACCTATCTGAGGGAAAATCATTTGGTGTC	1454
Qy	22	ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleIysTyrGlyVal	41
Db	1455	GTAGTCUGAGACCGGTGCTGTTTTCCACCACCAATGCTCGAAATAATTGTTATGACCGGT	1514
Qy	42	AspAspValThrAspGluGluMetGluArgAlaAlaAargGluAlaAsnAlaItyrAspPhe	61
Db	1515	GGAAATGTAACCATGGATGAGATAAAGAAGCTGTCAAAGAGGCCAACGGCTATGAGTTT	1574
Qy	62	IleMerClnPheProAsnLysPheAsnThrLeuValGlyGlyGlyGlyAlaGlnMetSer	81
Db	1575	ATCATGAATATCCACAGAATTTTGACCCTGTGTGGAGAGAGAGGGCCCCAGCTGAGT	1634
Qy	82	GlyGlyGlnLysGlnArgIleAlaIleAlaAargAlaLeuValAargAsnProLysIleLeu	101
Db	1635	GSITGGGCAGAAGCAGAGAGATCGCCATTGTCACTGCGTCCCTGCTTCGAACCCCAGATCCTT	1694
Qy	102	IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla	121
Db	1695	CTGCTGGATGAGGCCACGTCAGCATTTGGACACAGAAGTCGAAGCTCAGGTACAGGCAGCT	1754
Qy	122	LeuGlnLysAlaSerLysGlyValGtgThrIleValValAlaHisArgLeuSerThriIle	141

Db 1695 CTGCTGGATGAGCCAGCTCAGCATTTGGACACAGAAAGTGAAGCTGAGGTACAGGCAGCT 1754
Qy 122 LeuGluLysAlaSerLysGlyArgThrThrIleValAlaHisArgLeuSerThrIle 141
Db 1755 CTGGATAAGCCAGAGAGCCGCGACCACTTGTGATAGACACAGCACTGTCTACGGTC 1814
Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
Db 1815 CGAAATGACAGATGTCATCGCTGGTTGAGATGGAGTAATTTGGAGCAAGAGCCAC 1874
Qy 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuVal----- 175
Db 1875 AGCGAACTGATGAAGAGGAGGCTGACTTCAAACTTGTCAACATGCAGACATCAGGA 1934
Qy 176 -----MetSerGlnAspIleLysLysAlaAspGluGlnMetGluSerMetThrTyr 192
Db 1935 AGCCAGATCCAGTCAGAGAAATTTGAATTAATGATCAAAAGCTGCCATAGAAATGGCC 1994
Qy 193 SerThrGluArgLysThrAsnSerLeuProLeuHisSerValLysSerIleLys---Ser 211
Db 1995 CCAATGGCTGGAAATCTGCCTATTATTAGGCATTCTACTCAGAAACCTTTAAAAATTC 2054
Qy 212 AspPheIleAspLysAla---GluGluSerThrGlnSerLysGluIleSerLeuProGlu 230
Db 2055 CAAATGTGTGAGAGAGCCCTGATGTGAAACCGATGGACTTGAACAAATGTGCCACCA 2114
Qy 231 ValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTrpProPheValValLeuGly 250
Db 2115 GTCTCTCTTCTGAAGTCTCGAAATCGAATAAAACAGATGGCCCTACTTTGTCTGGGA 2174
Qy 251 ThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePheAlaLys 270
Db 2175 ACAGTATGTCCTATGCCATGGGGCTTCAGCCGGCATTTTCAGTCATATCTCAGAG 2234
Qy 271 IleIleThrMetPheGlyLeuAsnAspLysThrThrLeuLysHisAspAlaGluIleTyr 290
Db 2235 ATCATAGCGATTTTGGACAGCGCATGATGTCAGTGAAGCAGAGTGCACCATATTC 2294
Qy 291 SerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMetGlnGlyLeu 310
Db 2295 TCTTTGATTTCTATTCTGGGAATATTTCTTTTACTTTCTCTCTCTCTCTCTCTCT 2354
Qy 311 PheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAlaPheLysAla 330
Db 2355 ACCTTTGGGAAAGCTGCGAGATCTCCACAGAGAGCTCGGTCTCAATGGCTTTTAAAGCA 2414
Qy 331 MetLeuTyrGlnAspIleAlaTrpPheAspGluLysGluAsnSerThrGlyGlyLeuThr 350
Db 2415 ATGCTAAGACAGACATAGCTGGTTGATGACCATATAAACAAGTACTGCTGCACTTTCT 2474
Qy 351 ThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyValAlaThrGlySerArgIleGlyVal 370
Db 2475 ACAAGACTTGCACAGATGCTGCCAAGTCCCAAGGAGCCACAGAACCCAGGTTGGCTTTA 2534
Qy 371 LeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIleTyrGlyTyr 390
Db 2535 ATTGCACAGAAATAGCTAACCTTGGAACTGGTATTATCATATCATATTTATCTACGGTTGG 2594
Qy 391 GluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGlyMetIleGlu 410
Db 2595 CAGTTAACTTATGCTATTAGCAGTTGTTCCAAATTATTGCTGTGCAGGAATTTGTGA 2654
Qy 411 ThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHisAlaGlyLys 430
Db 2655 ATGAAATTTGTGTGCTGGAAATGCCAAAAGAGATAAAAAAGAACTGGAAGCTGCTGAAG 2714
Qy 431 IleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArgGluLysAla 450
Db 2715 ATTGCACAGAGCAATAGAAATATATAGACAGTTGTCTTTGACCCAGGAAGAAA 2774
Qy 451 PheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSerLysLysAla 470
Db 2775 TTTGAATCAATGATGTTGAAAAATTTGATGGACCTTACAGGAATTTCTGTGCAGAGGCA 2834

Qy 471 GlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAlaTyrAlaAla 490
Db 2835 CACATCTATGGAATTTACTTTTAGTATCTCACAGCAATTTATGATTTTTCCTATGCCGT 2894
Qy 491 GlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGluLysMetPhe 510
Db 2895 TGTTTTCGATTTGGTGCATATCTCATTTGTGAATGACATATCGCTTTCAGAGATGTTATT 2954
Qy 511 IleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeuValLeuAla 530
Db 2955 CTGGTGTTTTCTGCAATTTGTTTGGTGCAGTGGCTCTAGGACATGCCAGTTCATTGCT 3014
Qy 531 ProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeuGluLysLys 550
Db 3015 CCAGCATATGCTAAAGCTTAAGCTGTCTGCAGCCCACTTATTCTGCTGTTTCAAGACAA 3074
Qy 551 ProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGluGlyAsnLeu 570
Db 3075 CTTCTGATTTGACAGTACAGTGAAGAGGGCTGAGAGCTGATAAATTTGAAGGAATATA 3134
Qy 571 GluPheArgGluValSerPhePheTyrProCysArgProAspValPheIleLeuArgGly 590
Db 3135 ACATTTAATGAAGTCTGTTCAACTATCCACCCGAGCAACGTCCTCAGTGTCTCAGGG 3194
Qy 591 LeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSerGlyCysGly 610
Db 3195 CTGAGCTTGGAGTGAAGAAAGCCGACACTAGCCCTGGTGGCGACAGTGGCTGTGG 3254
Qy 611 LysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGlnGlyValLeu 630
Db 3255 AAGACACGGTGTCTCAGCTCTCTGGAGCGGTCTTACGACCCCTGGCGGGACAGTGT 3314
Qy 631 PheAspGlyValAspAlaLysGluLeuAsnValGlnTrpLeuArgSerGlnIleAlaIle 650
Db 3315 CTCGATGTCTAAGAGCAAGAAACTCAATGTCTCAGTGGCTCAGAGCTCAACTCGGAATC 3374
Qy 651 ValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAlaTyrGlyAsp 670
Db 3375 GTGCTCAGGAGCTTATCTCTATTGACTGCAGCAATTCGAGAAATATTGCTTATGGAG 3434
Qy 671 AsnSerArgValValProLeuAspGluIleLysGluAlaAlaAsnAlaAlaAsnIleHis 690
Db 3435 AACAGCCGGTGTATCATCAGGATGAATTTGAGTGCAGCCAAAGCTGCCAACATACAT 3494
Qy 691 SerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLysGlyAlaGln 710
Db 3495 CTTTTCATCGAGAGCTTACCCCAAAATATGAACACAGTGGGAGATAAGGGGACTCAG 3554
Qy 711 LeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGlnLysProLys 730
Db 3555 CTCTCAGAGGTCAAAAAACAGAGGATTTGCTATTGCCGAGCCCTCATCAGACAACTCAA 3614
Qy 731 IleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLysValValGln 750
Db 3615 ATCTCTCTGTTGGATGAAGCTACATCAGCTCTGGATCTGAAAGTGAAGAGTTGTCCAA 3674
Qy 751 HisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHisArgLeuSer 770
Db 3675 GAAGCCCTGGACAAAGCCAGAGAGGCCGACCTGCTGCTGATTGTTGCTCACCGCTGTC 3734
Qy 771 AlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLysGluGlnGly 790
Db 3735 ACCATCCAGATGTCAGACTTAATAGTGTGTTTCAGAAATGGAGAGTCCAGAGCATGGC 3794
Qy 791 ThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsnAlaGlnSer 810
Db 3795 ACGCATCAGCAGCTGCTGGCACAGAAAGCATCTATTATTTTCAATGCTCAGTCTCCAGGCT 3854

RESULT 11

US-10-101-433A-1

; Sequence 1, Application US/10101433A

; Publication No. US20030119726A1

GENERAL INFORMATION:
APPLICANT: Hanscom, Sara
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
FILE REFERENCE: G00307/70019
CURRENT APPLICATION NUMBER: US/10/101,433A
PRIORITY FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/277,095
PRIORITY FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 3852
TYPE: DNA
ORGANISM: Macaca mulatta
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3852)
US-10-101-433A-1

Alignment Scores:
Pred. No.: 2,13e-232 Length: 3852
Score: 2441.00 Matches: 465
Percent Similarity: 76.73% Conservative: 168
Best Local Similarity: 56.36% Mismatches: 174
Query Match: 59.84% Indels: 18
DB: 15 Gaps: 5

US-09-873-409-2 (1-813) x US-10-101-433A-1 (1-3852)

Qy	2	ValAspGluuAsnAspIleArgAlaLeuAsnValArgHisIstYrArgAspHisIleGlyVal	21
Db	1366	GTTCAGACAGGATATTAGGACCAATAAAGTAAAGTTTCTACGGGAATCATCGGTGTG	1425
Qy	22	ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAnlleLysTyrGlyArg	41
Db	1426	GTGAGTCAGGAACCTGTATTGTGTCACCAAGTACGCTGAAACATTTCGTATGTGGT	1485
Qy	42	AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe	61
Db	1486	GAAGATGTCACCATGATGAGATTGAGAAAGCTGTCAAGGAAGCAATGCTATGACTTT	1545
Qy	62	IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer	81
Db	1546	ATCATGAACCTGCTCAGAAATTTGACACCTGTGTGGAGAGAGAGGGCCAGCTGAGT	1605
Qy	82	GlyGlyGlnLysGlnArgIleAlaAlaAlaAlaLeuValArgAsnProLysIleLeu	101
Db	1606	GGTGGCAGAGCAGAGATGCCATTGCAAGTGGCTGTTCGACCCCAAGATCCTC	1665
Qy	102	IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla	121
Db	1666	CTGCTGGACGAGGCCACCTCAGCCTTGACACAGAAAGTGAAGCAGTGGTTCAGGTGCT	1725
Qy	122	LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle	141
Db	1726	CTGGTAAGGCCAGAAAGGTCGACCACTTGTATGATAGCTCATCGTTGTCTACCGTT	1785
Qy	142	ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis	161
Db	1786	CCTAATGCCGACGTCATCGCTGGTTTCGATGATGAGTCAATTTGTGGAGAAAGGAATCAT	1845
Qy	162	AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGlnAspIle---	180
Db	1846	GATGAGCTCATGAAGAGAAAGGCAATTACTTCAAACTTGTCAACATGCACAGCAGGGA	1905
Qy	181	-----LysLysAlaAspGlu-----GlnMetGluSerMetThr	191
Db	1906	AATGAATTAATTAAGAAATGCAGCTGATGAATCAATCAAAAGTGAATGATACCTGGAA	1965
Qy	192	TyrSerThrGluArgLysThrAsnSerLeu-----ProLeuHisSerVal	206
Db	1966	ATGCTTTCACATGATTCAGGATCCAGTCTAATAAGAAAGATCCACTCGTAGGAGTGT	2025

Qy	207	LysSerIleLysSerAspPheIleAspLysAlaGluGluSerThrGlnSerLysGluIle	226
Db	2026	CGTGGATCACAGGCCAA-----GACAGAAAGCTTAGTACCAAGAGGCTCTGGATGA	2079
Qy	227	SerLeuProGluValSerLeuLysIleLeuLysLeuAsnLysProGluTrpProphe	246
Db	2080	AGTATACCTCCAGTTTCCTTTTGGAGATTATGAAGCTAAATTAATTAATGAGTCCCTT	2139
Qy	247	ValValLeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIle	266
Db	2140	TTTGTGTTGTTGTTGTCGCAATTAATAATGGAGGCTGCAACCCAGCATTTGCAGTA	2199
Qy	267	IlePheAlaLysIleIleThrMetPhe---GlyAsnAsnAspLysThrThrLeuLysHis	285
Db	2200	ATATTTTCAAAGATTATAGGATTTTACAAAGAAATGATGATCCCGAAACCAACAGCAG	2259
Qy	286	AspAlaGluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyr	305
Db	2260	AATAGTAACCTGTTTTCATCTATTGTTTGTAGTCTTGGATTGTTCTTTTATACATT	2319
Qy	306	PheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHis	325
Db	2320	TTCTTTTCAAGGCTTCATTTGGCAAGCTGGAGAGATCTCCACCAAGCGGCTCCGATAC	2379
Qy	326	LeuAlaPheLysAlaMetLeuTyrGlnAspIleAlaTrpPheAspGluLysGluAsnSer	345
Db	2380	ATGTTTTCGATCCATGCTCAGACAGGATGAGTGGTGTGATGACCTTAAACACACC	2439
Qy	346	ThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGly	365
Db	2440	ACTGGAGCATGACTACCAAGCTCGCAATGATGCTGCTCAAGTTAAAGGGGCTATAGGT	2499
Qy	366	SerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSer	385
Db	2500	TCAGGCTGCTATAATATCCAGAAATATAGCAAAATCTTTGGGACAGAAATATATATCC	2559
Qy	386	PheIleTyrGlyTrpGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaVal	405
Db	2560	TTAATCTATGTTGGCACTGACACCTGTTACTCTTAGCAATTTGATCCCATCATGCAATA	2619
Qy	406	ThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeu	425
Db	2620	GCAGGAGTTGTTGAATGAATAATGTTGCTGGCAAGCACTGAAAGATAGAAAGAACTA	2679
Qy	426	LysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeu	445
Db	2680	GAAGTGTCTGGGAAGATCGCTACTGAAGCAATAGAAACTTCGGAAGTGTGTTCTTTG	2739
Qy	446	ThrArgGluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsn	465
Db	2740	ACTCAGAGCAGAGAGTTTGAACATATGATGATCAGAGTTTGCAGGTACCATCAGAAAC	2799
Qy	466	ThrSerLysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyr	485
Db	2800	TCCTTGGAGAAAGCACACATCTTTGGAATCAGTTTTCCTTCAACCAGGCAATGATGAT	2859
Qy	486	PheAlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThr	505
Db	2860	TTTTCCTATGCTGATGTTTCCGGTTTGGAGCTACTTGGTGGCACAATAGTCTCATGAGC	2919
Qy	506	ProGluGlyMetPheIleValPheThrAlaIleAlaTyrGlyValMetAlaIleGlyLys	525
Db	2920	TTTGAAGATGTTCTGTAGTATTTTCAGCTGTGTTCTTTGGTGGCCATGCGCGGGGCA	2979
Qy	526	ThrLeuValLeuAlaProGluTyrSerLysAlaLysSerGlyValaAlaHisLeuPheAla	545
Db	2980	GTCACTTTCCTGCTCTGACTATGCCAAAGCCAAAGTATCAGACGCCCAATCATCATG	3039
Qy	546	LeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThr	565
Db	3040	ATCATTTAAAGAAACCCCTTTGATTGACGTACAGACAGAGAGGCTTAAGCGGAACCA	3099

QY 267 IlePheAlaIleValLeuThrMetPhe---GlyAsnAspAspLysThrLeuLysHis 285
 DB 2290 ATATTTTCRAAGATTATAGGATTTTACAGAAATGATGATGCCGAAACAAAACGACAG 2349
 QY 286 AspaLaGluIleIleValPheValIleLeuGlyValIleCysPheValSerTyr 305
 DB 2350 AATAGTAATCTGTTTCTCACTATTGTTCTGATCTTCTGCAATGTTCTTTTATTACATT 2409
 QY 306 PheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHis 325
 DB 2410 TTCCTTCAGGCTTCACATTGGCAAGCTGGAGATCCTCCACCAAGCGGCTCCGATAC 2469
 QY 326 LeuAlaPheLysAlaMetLeuTyrGlnAspIleAlaTrpPheAspGluLysGluAsnSer 345
 DB 2470 ATGGTTTCCGATCCATCCTCAGACAGATGAGCTGTTTGTGATGACCTTAAACACACC 2529
 QY 346 ThrGlyGlyLeuThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGly 365
 DB 2530 ACTGAGCAATTGACTACCAAGCTCGCCCAATGCTGCTCAAGTTAAAGGGGCTATAGGT 2589
 QY 366 SerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSer 385
 DB 2590 TCCAGGCTTCATATTAATACCAAGATATACCAATCTTGGACAGGAATAATATATACC 2649
 QY 386 PheIleTyrGlyTrpGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaVal 405
 DB 2650 TTAATCTATGTTGGCAACGACATGTTACTCTTAGCAATGTACCCATCATTTGCAATA 2709
 QY 406 ThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeu 425
 DB 2710 GCAGAGTGTGTAATGAAATGTTGCTGCAAGCAAGCACTGAAAGATAGAAAGAACTA 2769
 QY 426 LysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeu 445
 DB 2770 GAAGTGCTGGAGAGATGCTACTGAAGCAATAGAAAACCTTCGAACTGTTGTTCTTTG 2829
 QY 446 ThrArgGluLysAlaPheGluMetTyrGluGluMetLeuGlnThrGlnHisArgAsn 465
 DB 2830 ACTCAGGACGAGAGTTTGAACATATGATGATGATGATGATGATGATGATGATGATGATG 2889
 QY 466 ThrSerLysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyr 485
 DB 2890 TCTTTGAGGAAGCACACATCTTTGGATACGTTTCTTCTTCCAGCAGCAATCATGTAT 2949
 QY 486 PheAlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThr 505
 DB 2950 TTTCTCTATGCTGGATGTTTCCGTTTGGAGCCTACTTGGTGGCACATAGTCTCATGAGC 3009
 QY 506 ProGluGlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLys 525
 DB 3010 TTTGAGGATGTTCTGTTAGTATTTTACAGTCTGTTGTTGTTGTTGTTGTTGTTGTTG 3069
 QY 526 ThrLeuValLeuAlaProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAla 545
 DB 3070 GTCAGTTCTATGCTCTCTGACTATGCCAAAGCCAAAGTATATCCAGCGCCCATCATCATG 3129
 QY 546 LeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThr 565
 DB 3130 ATCATGAAACACCCCTTGAATGACAGCTACGACAGAGAGCCCTTAAGCCGAAACACA 3189
 QY 566 CysGluGlyAsnLeuGluPheArgGluValSerPheTyrProCysArgProAspVal 585
 DB 3190 TTGGAAGGAAATGTCACATTTAATGAAGTTGTTTCACTATCCACCGCCACTGGACATC 3249
 QY 586 PheIleLeuArgGlyLeuSerLeuIleGluArgGlyLysThrValAlaPheValGly 605
 DB 3250 CCAGTGCTTCAGGGCTGAGCTGGAAGTGAAGAGGGCCAGACGCTGGCCCTGCTGGCC 3309
 QY 606 SerSerGlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProVal 625
 DB 3310 AGCAGTGCTGTTGGGAAGAGCAGCAGCTGTTGCTGAGCTCTGAGAGCGGTTCTATGACCCCTTG 3369

QY 626 GlnGlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnTrpLeuArg 645
 DB 3370 GCCGGGAAGTCTGCTTGAAGCAAGAAATPAAACCACTGATGATGTTCTAGTGGCTCCGA 3429
 QY 646 SerGlnIleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsn 665
 DB 3430 GCACACTGGGCTGCTGTTGCCAGGAGCCATCTCTGTTGACTGTCAGCATTTAGTGAGAAC 3489
 QY 666 IleAlaTyrGlyAspAsnSerArgValValProLeuAspGluIleLysGluAlaAlaAsn 685
 DB 3490 ATTGCTTATGGAGAACACCGCGGTGGTGTCTCAGAGAGAGATCTGTAGGCGGACGCAAG 3549
 QY 686 AlaAlaAsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGly 705
 DB 3550 GAGGCCAATATACAGCCTTCATCGAGTCACTGCTTAATAAATATAGCACAGAGTAGGA 3609
 QY 706 LeuLysGlyAlaGlnIleSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeu 725
 DB 3610 GACAAAGGAACACTGAGTCTCTGTTGGTCCGAGAAACCAACGCAATGCCATGCTGCTGCTT 3669
 QY 726 LeuGlnLysProLysIleLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSer 745
 DB 3670 GTTAGACAGCCTCATATTTTGTCTTTTGGATGAAGCCACATCAGCTCTGGATACAGAAAGT 3729
 QY 746 GluLysValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValVal 765
 DB 3730 GAAAGAGTGTTCACAGAGCCCTTGGACAAAGCCAGAGAGCGGTACCTGCTGCTGCTGCTT 3789
 QY 766 ThrHisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLys 785
 DB 3790 GCTCAGCGCTGTCCACCATCCAGATGCGAGACTTAATAGTGTGTTTCAGAAATGCGAGA 3849
 QY 786 IleLysGluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeu 805
 DB 3850 GTCAGAGAGCAGCGGCACATCAGCAGCTGCTGGCCACAGAAAGGCATCTATTTTCAATG 3909
 QY 806 ValAsnAlaGlnSer 810
 DB 3910 GTCAGTGTCCAGGCT 3924

RESULT 13
 US-10-619-359A-3
 ; Sequence 3, Application US/10619359A
 ; Publication No. US20040077000A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STOCKER, PENNY J.
 ; APPLICANT: STEINEL-CRESPI, DOROTHY T.
 ; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
 ; FILE REFERENCE: G00307.70020.US
 ; CURRENT APPLICATION NUMBER: US/10/619,359A
 ; CURRENT FILING DATE: 2003-07-14
 ; PRIOR APPLICATION NUMBER: US 60/156,921
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/158,818
 ; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: US 09/672,810
 ; PRIOR FILING DATE: 2000-09-28
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 4195
 ; TYPE: DNA
 ; ORGANISM: Macaca fascicularis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (100)...(3949)
 US-10-619-359A-3

Alignment Scores:
 Pred. No.: 2,42e-232 Length: 4195
 Score: 2441.00 Matches: 465
 Percent Similarity: 76.73% Conservative: 168

Best Local Similarity: 56.36%			Mismatches: 174		
Query Match: 59.84%			Indels: 18		
DB: 17			Gaps: 5		
US-09-873-409-2 (1-812) x US-10-619-359A-3 (1-4195)					
QY	2	ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21			
DB	1465	GTGATGGACAGGATATTAGACATCAAGCAAGTAAAGTTTCTACGGGAAATCATCGGTGTG 1524			
QY	22	ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41			
DB	1525	GTGAGTCAGCAAGCTGTATTGTTGCCACACAGATAGCTGAAACAATTCGCTATGTGCTG 1584			
QY	42	AspAspValThrAspGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61			
DB	1585	GAAGATGTCACATGATGAGATGAGAAAGCTGTCAAGCAAGCCCAATGCTATGACTTT 1644			
QY	62	IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81			
DB	1645	ATCATGAACTGCTCAGAAATTTGACACCTTGGTTGGAGAGAGGGGCCCAAGCTGAGT 1704			
QY	82	GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101			
DB	1705	GGTGGCAGAAAGCAGAGGATCGCCATTCAGCTGCCCTGGTTCGCAACCCCAAGATCCTC 1764			
QY	102	IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121			
DB	1765	CTGCTGGACGAGCCAGCTCAGCCCTTGGACACAGAAGTGAAGCAGTGTTCAGGTGGCT 1824			
QY	122	LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141			
DB	1825	CTGGATAAGCCAGAAAGGTTCGACCAACCATTTGTGATAGCTCATCGTTTGTCTACGGTT 1884			
QY	142	ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161			
DB	1885	CGTAATGCCAGCTGATCGCTGGTTCGATGATGGAGTCATTTGTGAGAAAGGAATCAT 1944			
QY	162	AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGlnAspIle--- 180			
DB	1945	GATGAGCTCATGAAGAGAAGAGCCATTACTTCAAACTTGTCACAAATGCCAGACAGGGA 2004			
QY	181	-----LysLysAlaAspGlu-----GlnMetGluSerMetThr 191			
DB	2005	AATGAAATTAAGAAATGAGACCTGATGAATCCAAAGTGAAATTCATACCTTGGAA 2064			
QY	192	TyrSerThrGluArgLysThrAsnSerLeu-----ProLeuHisSerVal 206			
DB	2065	ATGCTCTTCATGATTCAGATCCAGTCTAATAAGAAAGATCCACTCGTAGAGTGTC 2124			
QY	207	LysSerIleLysSerAspPheIleAspLysAlaGluLysThrGlnSerLysGluIle 226			
DB	2125	CGTGGATCACAAGGCCAA-----GACAGAAAGCTTAGTACCAAGAGGCTCTGGATGAA 2178			
QY	227	SerLeuProGluValSerLeuLysIleLeuLysLeuAsnLysProGluTrpProPhe 246			
DB	2179	AGTATACCTCCAGTTTCTTTTGGAGGATATAGAGCTAAATTTAACTAGTGGCTTAT 2238			
QY	247	ValValLeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIle 266			
DB	2239	TTTGTTGTGGTGTATTTTGTGGCATTAATAATGGAGGCTCGAACCAACCATTTGCAATA 2298			
QY	267	IlePheAlaLysIleIleThrMetPhe---GlyAsnAsnAspLysThrThrLeuLysHis 285			
DB	2299	ATATTTTCAAGATATATAGGATTTTACAGAAATATGATGATGCCGAAACAAACGACAG 2358			
QY	286	AspAlaGluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyr 305			
DB	2359	AATAGTAATCTGTTTCACTATGTTTCTAGTCCCTTGGAAATGTTTCTTTTATTCATTT 2418			
QY	306	PheMetGlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHis 325			
DB	2419	TTCTTTCAGGGCTTCACATTTGGCAAGCTGGAGAGATCCTCACCAGAGCGGCTCCGATAC 2478			
QY	326	LeuAlaPheLysAlaMetLeuTyrGlnAspIleAlaTrpPheAspGluLysGluAsnSer 345			
DB	2479	ATGGTTTTCGGATCCATGCTCAGACAGGATGTGAGCTGTGTTGATGACCTAAACACACC 2538			
QY	346	ThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGly 365			
DB	2539	ACTGGAGCATTTGACTACCAAGGCTCCCAATGATGTCTCTCAAGTTTAAAGGGCTTATAGGT 2598			
QY	366	SerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSer 385			
DB	2599	TCAGGCTTGTCTATTAATACCCAGATATAGCAATCTTGGACAGGAATATATATATATCC 2658			
QY	386	PheIleTyrGlyTrpGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaVal 405			
DB	2659	TTAATCTATGTTGGCAACTGACACTGTCTCTTAGCAATTTGATCCCATCATTCGCAATA 2718			
QY	406	ThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeu 425			
DB	2719	GCAGGAGTTTGTGAATGAAATGTTGTCTGGACACAGACTGAAAGATTAAGAAAGAACTA 2778			
QY	426	LysHisAlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeu 445			
DB	2779	GAAGGTGCTGGGAAGATCGCTACTGAGCAATAGAAAACCTTCGGAACCTGTTGTTCTTTG 2838			
QY	446	ThrArgGluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsn 465			
DB	2839	ACTCAGGACGAGAGTGTGAACATATGATGATCAGAGTTTGCAGGTACCATACAGAAAC 2898			
QY	466	ThrSerLysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyr 485			
DB	2899	TCTTTGAGGAAGCACACATCTTTGGAATCAGCTTTCCTTTCACGCAGGCAATGATGAT 2958			
QY	486	PheAlaTyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThr 505			
DB	2959	TTTCTCTATGCTGGATGTTTCCGGTTTGGAGCTACTTGTGGGCACATAGTCTCATGAGC 3018			
QY	506	ProGluGlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLys 525			
DB	3019	TTTGAGGATGTTCTGTTAGTATTTTTCAGCTGTGTTTGTGGTCCATGCGCGGGGCAA 3078			
QY	526	ThrLeuValLeuAlaProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAla 545			
DB	3079	GTCACTTCATTTGCTCTCTGACTATGCCAAGCAAGATATCAGCAGCCACATCATCATG 3138			
QY	546	LeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThr 565			
DB	3139	ATCATTGAAAGAACCCCTTTGATTGACAGCTACAGCACAGAAAGGCTTAAAGCCGACACA 3198			
QY	566	CysGluGlyAsnLeuLeuPheArgGluValSerPhePheTyrPcCysArgProAspVal 585			
DB	3199	TTGGAAGGAAGTGCACATTTAATGAAGTTGTATTCAACTATCCACCCGACTGGACATC 3258			
QY	586	PheIleLeuArgGlyLeuSerSerIleGluArgGlyLysThrValAlaPheValGly 605			
DB	3259	CCAGTGTCTCAGGGGCTGAGCTCGAAAGTGAAGAGGCGCCAGACGCTGGCGCTGTGGGC 3318			
QY	606	SerSerGlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProVal 625			
DB	3319	AGCAGTGGCTGTGGAGAGAGACCGGTGCTCCAGCTTCTTGGAGCGGTTCTATGACCCCTTG 3378			
QY	626	GlnGlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnTrpLeuArg 645			
DB	3379	CGCGGGAAGTGTGCTGTGACGGCAAGAAATAAAGCAACTGAATGTTTCAGTGGCTCCGA 3438			
QY	646	SerGlnIleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsn 665			
DB	3439	GCACACCTGGGCATCGTGTCCAGAGGCCCATCTCTTGTGACTGAGCATTTAGTGAGAAC 3498			
QY	666	IleAlaTyrGlyAspAsnSerArgValValProLeuAspGluIleLysGluAlaAlaAsn 685			
DB	3499	ATTGCTATGGAGACAACAGCGCGGTGTGTGCACAGGAAGAGATCTGTGAGGCGGACCAAG 3558			

Qy 686 AlaAlaAsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGly 705
Db 3559 GAGCCCAATATACAGCGCTTCACTGAGTCACTGCTTAATAATATACACAGAGTAGGA 3618
Qy 706 LeuLysGlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeu 725
Db 3619 GACAAGAGAACTCAGCTCTCTGTGGTGGCCAGAAAACAGCCGATTTGCCATAGCTCGTGCCTT 3678
Qy 726 LeuGlnLysProLysIleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSer 745
Db 3679 GTTAGACAGCGCTCATATTTGCTTTGATGAGCCACATCAGCTCTGGATACGAAGGT 3738
Qy 746 GluLysValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValVal 765
Db 3739 GAAAGGGTTGTCAGAGAGCCCTGCACAAAGCCAGACAGAGCCGCTACCTGCTGATTT 3798
Qy 766 ThrHisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLys 785
Db 3799 GCTCAGCGCTGTCCACCATCCAGATGCAGACTTAATAGTGGTTCAGATGGCGGA 3858
Qy 786 IleLysGlnGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeu 805
Db 3859 GTCAAGGAGCAGCGCCACACATCACAGCTGCTGCCACAGAAAGCATCTATTTTCAATG 3918
Qy 806 ValAsnAlaGlnSer 810
Db 3919 GTCAGTGTCCAGGCT 3933
RESULT 14
US-09-769-097-1
; Sequence 1, Application US/09769097
; Patent No. US20020055128A1
; GENERAL INFORMATION:
; APPLICANT: Kimberly Anne Brun
; APPLICANT: Richard James Chenery
; APPLICANT: Harma Ellens
; APPLICANT: John Anthony Feild
; APPLICANT: Lin Yue
; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: ENCODING RAT MDRIA AND SCREENING METHODS THEREOF
; FILE REFERENCE: GP-50009-C2
; CURRENT APPLICATION NUMBER: US/09/769,097
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/208,809
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 09/156,800
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US99/20770
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4369
; TYPE: DNA
; ORGANISM: RATTUS RATTUS
US-09-769-097-1
Alignment Scores:
Pred. No.: 2,58e-232 Length: 4369
Score: 2441.00 Matches: 470
Percent Similarity: 77.04% Conservative: 164
Best Local Similarity: 57.11% Mismatches: 175
Query Match: 59.84% Indels: 14
DB: 9 Gaps: 5
US-09-873-409-2 (1-812) x US-09-769-097-1 (1-4369)
Qy 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
Db 1684 ATCCAGCGACAGGACATCAGACCATCAATGTGAGGTATCTTCGGGAAATCATTTGGGGTG 1743
Qy 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnIleLysTyrGlyArg 41

Db 1744 GTGAGTCAGGAACCGGTGCTGTTGTTGCCACCAATTTCCGAAAAACATTCGCTATGCGCGA 1803
Qy 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 1804 GAAAGCTCACCATGTAGATAGAGAAGCTGTCAAGGAAGCCATTCCTATGATTTTC 1863
Qy 62 IleMetGluProAsnLysPheAsnThrLeuValGlyGlyGlyAlaGlnMetSer 81
Db 1864 ATCATGAAACTGCCCCACAAATTTGACACCTGTTGTTGAGAGAGGGCGCAGCTGAGT 1923
Qy 82 GlyGlyGlnGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
Db 1924 GGGGGACAAACAGAGGATCCCATTTGCCGGGCCCTGTCCGCAACCCCAAGATCCCT 1983
Qy 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
Db 1984 TTGTTGATGAGCCACAGCTCAGCTTGGACACAGAAAGCGGCGGTGTTTCAGGCCGCT 2043
Qy 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141
Db 2044 CTGGATTAAGCTTAGAAGCGCGACCATTTGTGATAGCTCACCGCTTGCTACAGTT 2103
Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
Db 2104 CGCAATGCTGACGTCATTCCTGCTGTTGATGCTGTTGATGCTGAGGAGCAAGAAATCAT 2163
Qy 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGln 178
Db 2164 GATGAGCTCATGAGAGAGAAAGAAATTTTACTTCAAACTTGTCTGATGACTCAGACAGCA 2223
Qy 179 ---AspIleLysLysAlaAspGluGlnMetGluSer 191
Db 2224 AATGAAATTTGAATTAGGAATAGAGCTTGTGAATCTTAAGACGGAATGATTAATGTGGAC 2283
Qy 192 TyrSerThrGluArgLysThrAsnSerLeu 209
Db 2284 ATGTCTTCAAAAGATTCGGGATCCAGTCTAATAAGAAAGATCACTCGCAAAAGCATC 2343
Qy 210 LysSerAspPheIleAspLysAlaGluGluSerThr 228
Db 2344 CTGGGCCCATCATGATCAACAGCGGGAACCTTACCAAGAGGCTCTGATGACGACGTA 2403
Qy 229 ProGluValSerLeuLysIleLeuLysLeuAsnLysProGluTyrProPheValVal 248
Db 2404 CTTCCAGCTTCTTTTGGCGGATCTCTGAAGTTGAATTCAACTGAATGGCTTAATTTGTG 2463
Qy 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
Db 2464 GTTGGTGTATTTGTGCCATAATAATGAGGCTTGCACCAAGAGCATTTCTCCATAATATT 2523
Qy 269 AlaLysIleIleThrMetPheGlyAsnAsnAspLysThrThrLeu 287
Db 2524 TCAGAGTTGTAGGGGTTTTTACAAAAAATGACACCCCTGAAATCCAGCGGAGAAACAGC 2583
Qy 288 GluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMet 307
Db 2584 AACTGTGTTTCTTATTGTTCTGATCCTTGGGATCATCTCTTTTATTACGTTTTTCTTT 2643
Qy 308 GlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAla 327
Db 2644 CAGGGCTTCACATTTGGCAAGCTCGAGAGATCTCTCACCAGCGACTCCGATACATGGTC 2703
Qy 328 PheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAspGluLysGluAsnSerThrGly 347
Db 2704 TTCAAAATCCATGCTGAGACAGGACATAAGCTGGTTGATGCCCTTAAACCAACCAACAGGA 2763
Qy 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyValaThrGlySerArg 367
Db 2764 GGGCTGACCAACAGGCTTCCCAATGACGCTGTCAAGTGAAGGGGCTACAGGGTCTAGG 2823
Qy 368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
Db 2824 CTTGCTGTTATTATCCAGAAACATAGCAAAATCTTGGGACAGGATCATCATATCTCCCTGATC 2883

QY 388 TyrGlyThrGluMetThrPheLeuLeuSerIleAlaProValLeuAlaValThrGly 407
Db 2884 TACGGCTGGCAATGTGACCTTTACTCCCTAGCAATTTGTTCCCATCATCTGTATAGCAGGA 2943
QY 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHis 427
Db 2944 GTGGTTGAAATGAAATGTTGTCTGCACAGCGCTCAAGAGATAAGAGAACTAGAAGCT 3003
QY 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArg 447
Db 3004 TCTGGGAAGATCGCTACAGAGCAATTTGAAACTTTCCGCACTGTCTCTTTGACTCGG 3063
QY 448 GluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
Db 3064 GAGCAGAAGTTGAAACTATGATGATGCCAGAGCTTCAGATACCAACAGAAATGCTTTG 3123
QY 468 LysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAla 487
Db 3124 AAGAAAGCGCAGCTCTTTGGATCACTTTCTCTTCCAGCCGCAATGATTTCTCC 3183
QY 488 TyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGlu 507
Db 3184 TATGCTGTGTTTCCGGTTGATGCTACTTGTGGCAGGAGACTCATGACATTTGAA 3243
QY 508 GlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeu 527
Db 3244 AATGTTCTGTATTCTCAGCTATTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3303
QY 528 ValLeuAlaProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547
Db 3304 TCATTCGCTCTGACTACCGGAAGCAAGTCTCGGCATCCCATCATCATCAGGATCAT 3363
QY 548 GluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGlu 567
Db 3364 GAGAAATCCCTGAGATTGACAGCTACAGCAGGAGGCTTGAGGCTTAATATGTTGAA 3423
QY 568 GlyAsnLeuGluPheArgGluValSerPhePheTyrProCysArgProAspValPheIle 587
Db 3424 GGAATGTGAATTTAATGAGTCATGTTCACTATCCACCGCCGCCCACTCCCGAGTG 3483
QY 588 LeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSer 607
Db 3484 CTTGAGGGCTGAGCTTAGAGTGAGAGAGGCGAGACGCTGGCCCTCTGCGGACAGCT 3543
QY 608 GlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGly 627
Db 3544 GGCTGCGGGAAGATACAGTGTGCTCAGCTGCTTGTAGCGCTTCTATGACCCCATGCCGGA 3603
QY 628 GlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnTyrLeuArgSerGln 647
Db 3604 ACAGTGTCTAGATGCGAAGAAATAAAGCACTCAATGTCAGTGGCTCCGCGCCAC 3663
QY 648 IleAlaIleValProGlnProValLeuPheAsnCysSerIleAlaGluAsnIleAla 667
Db 3664 CTGGGCTATTGTGCCAGGAGCCATCTCTGTTGACTGCAGCATGCCGAGAACATTGCC 3723
QY 668 TyrGlyAsnAsnSerArgValValProLeuAspGluIleLysGluAlaAlaAlaAla 687
Db 3724 TACGGAGACAACAGCGCTGTGCTGCTCTCATAGGAGATCTGAAGAGCAGCCAAAGAGGCC 3783
QY 688 AsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLys 707
Db 3784 AACATCCACCACTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3843
QY 708 GlyAlaGlnLeuSerGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuGln 727
Db 3844 GGGACTCAGCTGTGGGCGGAGAGAGCAGCGCATCGCCATCGCGCGCGCTCTGCTCAGA 3903
QY 728 LysProLysIleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLys 747
Db 3904 CAGCCTCACATCTTATTCTGATGAGCGACATCAGCTCTGATACCGAGAGTGAAG 3963

QY 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHis 767
Db 3964 GTCTGTCAGGAGCGCTCGACAAAGCCAGGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 4023
QY 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 4024 CGCTGTCCACCATCCAGACCGCAGACTGATCGTGTGATTCAGACCGCCAGCTCAAG 4083
QY 788 GluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsn 807
Db 4084 GAGCAGCGCAGCCACCGACGCTGCTGCCCGAGAAAGCACTATTCTGATGCTGCTGCT 4143
QY 808 AlaGlnSer 810
Db 4144 GTGCAAGCT 4152

RESULT 15
US-09-769-097-3
; Sequence 3, Application US/09769097
; Patent No. US20020055128A1
; GENERAL INFORMATION:
; APPLICANT: Kimberly Anne Brun
; APPLICANT: Richard James Chenery
; APPLICANT: Harma Ellens
; APPLICANT: John Anthony Feild
; APPLICANT: Lin Yue
; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: GP-50009-C2
; CURRENT APPLICATION NUMBER: US/09/769,097
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/208,809
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 09/156,800
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US99/20770
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4425
; TYPE: DNA
; ORGANISM: RATTUS RATTUS
US-09-769-097-3

Alignment Scores:
Pred. No.: 2,63e-232 Length: 4425
Score: 2441.00 Matches: 470
Percent Similarity: 77.04% Conservative: 164
Best Local Similarity: 57.11% Mismatches: 175
Query Match: 59.84% Indels: 14
Gaps: 5

US-09-873-409-2 (1-812) x US-09-769-097-3 (1-4425)

QY 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
Db 1684 ATCCAGCGACAGGACATCAGGACCATCATGTGAGTATCTCGCGGAAATCATTTGGGCTG 1743
QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
Db 1744 GTGAGTCAGGAACCGCTGCTTTGCCACCACCAATTCGGAACCAATTCGCTATGCCGA 1803
QY 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 1804 GAAACGTCACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1863
QY 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
Db 1864 ATCATGAACTGCCCCCAAAATTTGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1923
QY 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101

Db 1924 GGGGACAGAAACAGAGGATCGCCATTGCCCCGGGCCCTGGTCCGCAACCCCAAGATCCTT 1983
Qy 102 ILeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
Db 1984 TTGTGTGATGAGGCGCAGTCAAGCTTGGACACAGAAAGGAGGCGGTTCAGGCGGCT 2043
Qy 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaAlaHisArgLeuSerThrIle 141
Db 2044 CTGGATAGGCTAGAGAGGCGGACCAACCATTTGTGATAGCTCACCGTTGTCTACAGTT 2103
Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
Db 2104 CGCAATCTGATGTCATTTGCTGGTTTGGATGGTGGTGTCTATTGTGGAGCAAGGAATCAT 2163
Qy 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGln----- 178
Db 2164 GATGAGCTCATGAGAGAGAGGAATTTACTTCAAACTTGTCTAGTCTAGACAGCAGGA 2223
Qy 179 ---AspIleLysLysAlaAspGluGlnMetGluSer-----MetThr 191
Db 2224 AATGAATTTCAAGATTTAGGAATGAAGCTTGTGAATCTAAAGAGGAATTTGATATGTGGAC 2283
Qy 192 TyrSerThrGluArgLysThrAsnSerLeu-----ProLeuHisSerValLysSerIle 209
Db 2284 ATGTCTTCAAGAGATTCRGATCCAGTCTAATTAAGAGAGAGATCAACTCGCAANAGCATC 2343
Qy 210 LysSerAspPheIleAspLysAlaGluGluSerThr---GlnSerLysGluIleSerLeu 228
Db 2344 CGTGGGCGACATGATCAAGACGGGGAACCTAGCACCAAGAGGCTCTGGATGACGACGTA 2403
Qy 229 ProGluValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTrpProPheValVal 248
Db 2404 CTTCCAGCTCTTTTGGCGGATCTCTGAAGTTGAATTCAACTGAATGGCCCTTATTTTGG 2463
Qy 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
Db 2464 GTTGTGTATTTTGTGCCATAATAAATGGAGGCTTGCAACACGACATTTCTCCATAATATTT 2523
Qy 269 AlaLysIleIleThrMetPheGlyAsnAsnAspLysThrThrLeu---LysHisAspAla 287
Db 2524 TCAGAGGTGTAGCGGTTTTTACAAAAAATGACACCCCTCAAAATCCAGCGGCGAGACAGC 2583
Qy 288 GluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMet 307
Db 2584 AACTGTGTCTTATTTGTTCTGATCTCTGGATCATCTTTCATAGCTTTTCTT 2643
Qy 308 GlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAla 327
Db 2644 CAGGGCTTCATTTGGCAAGCTGGAGAGATCTCACCAGGCGACTCCCATATACATGGTC 2703
Qy 328 PheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAspGluLysGluAsnSerThrGly 347
Db 2704 TTCAAATCCATGCTGACACAGACATTAAGTGTGTTGATGACCTTAAACACACACAGGA 2763
Qy 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
Db 2764 GCGCTGACCAAGCTTGCATAGCTGCTCAAGTGAAGGGGCTACAGGCTCTAGG 2823
Qy 368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
Db 2824 CTTCCTGTTATACCCAGACATAGCAAAATCTTGGACAGGCAATCATATCCCTGATC 2883
Qy 388 TyrGlyTrpGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGly 407
Db 2884 TACGGCTGGCAATTTGACACTTTTACTCTAGCAATTTGTTCCATTTGCTATAGCAGGA 2943
Qy 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnLeuLysHis 427
Db 2944 GTGGTTGAATGAATAATGTTGCTGGACCAAGCGCTGAAAGATAGAAAGGAAGTGAAGGT 3003
Qy 428 AlaGlyLysIleAlaThrGluAlaLeuGlnAsnIleArgThrIleValSerLeuThrArg 447
Db 3004 TCTGGAGAGATCGCTACAGAGCAATTTGAAACATTTTCGACTGTCTCTTTGACTCGG 3063

Qy 448 GluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
Db 3064 GAGCAGAAAGTTGAACATATGTATATCCAGAGCTTCCAGATACCATACAGAAATGCTTTG 3123
Qy 468 LysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAla 487
Db 3124 AAGAAAGGCGAGCTCTTTGGATCATCTTCTCTTCCATCCAGGCGCATGATGATTCTCC 3183
Qy 488 TyrAlaAlaGlyPheArgPheGlyAlaTyrIleuIleGlnAlaGlyArgMetThrProGlu 507
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Qy 508 GlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeu 527
Db 3244 ANTGTCTGTAGTATTCTCAGTATTCTTCTTGGTGCATGGCAGTGGGCGAGTCACT 3303
Qy 528 ValLeuAlaProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547
Db 3304 TCATTCTGCTCTCTGACTACGCAAGCCAAAGTCTCGGCATCCCATCATCATCAGGATCAT 3363
Qy 548 GluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGlu 567
Db 3364 GAGAAATCCCTGACATGACAGCTACAGCAGGAGGGCTTGAAGCCTAATATGTTGAA 3423
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Qy 608 GlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGly 627
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Qy 688 AsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLys 707
Db 3784 AACATCCACCATTTCTCATGACTCATGCTCTGAGAAATACACACAGAGTGGAGACAAA 3843
Qy 708 GlyAlaGlnLeuSerGlyGlyGlnArgLeuAlaIleAlaArgAlaLeuLeuGln 727
Db 3844 GGGACTCAGCTGCGGGCGGAGAGCGGCATCGGCATCGCGCGGCCCTCTGTCAGA 3903
Qy 728 LysProLysIleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLys 747
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Qy 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHis 767
Db 3964 GTCTGTCAGAGAGCGCTGGACAAAGCCAGGCGGCGGAGGCGGCTGATTTGATGTCGGCAC 4023
Qy 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 4024 GCGCTGTCCACCATCCGAAACCGAGACTTGATGCTGGTGTGATTCAGNACCGGCGAGGTCAAG 4083
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Qy 808 AlaGlnSer 810
Db 4144 GTGCAGGCT 4152

Search completed: June 25, 2004, 03:51:13
Job time : 994 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 24, 2004, 23:38:48 ; Search time 167 Seconds

(without alignments)
2698.324 Million cell updates/sec

Title: US-09-873-409-2

Perfect score: 4079

Sequence: 1 MYDENDIRALNRYHRDHIG.....QELLNRDIYFKLVNAQSVQ 812

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Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -LOCALIGN=200 -THR SCORE=pet -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

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- 3: /cgn2_6/prodata/2/ina/6A-COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2465.5	60.4	3924	4	US-09-023-655-1168 Sequence 1168, Ap
2	2465.5	60.4	3924	4	US-09-762-195-2 Sequence 2, Appli
3	2441	59.8	4186	4	US-09-672-810-1 Sequence 1, Appli
4	2441	59.8	4195	4	US-09-672-810-3 Sequence 3, Appli
5	2436	59.7	3988	4	US-09-762-195-1 Sequence 1, Appli
6	2436	59.7	4264	2	US-08-784-649A-1 Sequence 1, Appli
7	2436	59.7	4264	2	US-08-784-649A-5 Sequence 5, Appli
8	2436	59.7	4646	1	US-08-181-471-2 Sequence 2, Appli
9	2436	59.7	4646	4	US-09-023-655-1167 Patent No. 5206352
10	2436	59.7	4669	6	5206352-3 Sequence 1167, Ap
11	2436	59.7	8505	2	US-08-793-610-5 Sequence 5, Appli
12	2436	59.7	8630	4	US-09-306-417-1 Sequence 1, Appli

13	2436	59.7	8630	4	US-09-306-417-2 Sequence 2, Appli
14	2436	59.7	9318	2	US-08-793-610-6 Sequence 6, Appli
15	2413.5	59.2	4233	3	US-09-120-513-1 Sequence 1, Appli
16	2413.5	59.2	4233	3	US-09-450-105-1 Sequence 1, Appli
17	2412	59.1	4669	4	US-08-752-447-1 Sequence 1, Appli
18	2412	59.1	4669	4	US-09-316-167-1 Sequence 1, Appli
19	2412	59.1	4669	4	US-09-397-233-1 Sequence 1, Appli
20	2397	58.8	4669	2	US-08-583-276-18 Sequence 18, Appli
21	2280	55.9	2726	1	US-08-461-823-1 Sequence 1, Appli
22	1894	41.5	4175	4	US-09-749-340-3 Sequence 3, Appli
23	1690.5	41.4	4002	2	US-08-996-545-1 Sequence 1, Appli
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26	1690.5	41.4	4002	3	US-09-328-320-3 Sequence 3, Appli
27	1678.5	41.1	3512	4	US-09-749-340-7 Sequence 7, Appli
28	1661	40.7	4047	2	US-08-612-734B-1 Sequence 1, Appli
29	1618	39.7	4800	2	US-08-612-734B-3 Sequence 3, Appli
30	1617	39.6	2698	4	US-08-749-340-5 Sequence 5, Appli
31	1570.5	38.5	3924	1	US-08-395-246C-1 Sequence 1, Appli
32	1538.5	37.7	2681	4	US-09-749-340-8 Sequence 8, Appli
33	1474	36.1	4224	1	US-08-612-521-1 Sequence 1, Appli
34	1255.5	30.8	3909	1	US-08-232-537-1 Sequence 1, Appli
35	1223.5	30.0	3924	2	US-08-996-644-3 Sequence 3, Appli
36	1223.5	30.0	3924	3	US-09-352-552-3 Sequence 3, Appli
37	1223.5	30.0	3927	2	US-08-996-644-1 Sequence 1, Appli
38	1223.5	30.0	3927	3	US-09-352-552-1 Sequence 3, Appli
39	1172	28.7	6143	1	US-08-612-521-3 Sequence 3, Appli
40	1116.5	27.4	3792	4	US-09-351-224E-10 Sequence 10, Appli
41	1116.5	27.4	3792	4	US-09-677-682B-10 Sequence 10, Appli
42	1116.5	27.4	3792	4	US-09-677-682B-10 Sequence 10, Appli
43	1032.5	25.3	3999	4	US-09-351-224E-9 Sequence 9, Appli
44	1032.5	25.3	3999	4	US-09-677-682B-9 Sequence 9, Appli
45	1032.5	25.3	3999	4	US-09-677-682B-9 Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-09-023-655-1168

; Sequence 1168, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0001 US

; TELECOMMUNICATION INFORMATION:

2115	GTGTCCTTTCTGAAGGTCCTGAAGAACTGAATAAAACAGCAATGGCCCTACTTTGTCTGCTGGGA	2174
Qy	251 ThrLeuAlaSerValLeuIleuAsnGlyThrValHisProValPheSerIleIlePheAlaLys	270
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Qy	271 IleIleThrMetPheGlyAsnAsnAspLysThrThrLeuLysHisAspAlaGluIleTyr	290
Db	2235 ATCATACGCAATTTTGGACCGCGCGATGATGCGAGTCAGTCAGCAGACAGAGTGCACATATTC	2294
Qy	291 SerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMetGlnGlyLeu	310

	331	PheTyr-GlyArgAlaGlyLeuIleThrMetArgLeuArgHisLeuAlaPheLysAla	330
Qy		:::::	
D6	2355	ACGTTTGGGAAGACTGCAGATCTCCACAGAAGACTCGGTCATGGCTTTTAAGCA	2414
		:::::	
Qy	331	MetLeuTyrGlnAspileAlaTrpPheAspGluLysGluAsnSerThrGlyGlyLeuThr	350
		:::::	

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[illegible][illegible][illegible]

Qy	471	GlnIleIleIleGlySerCysYsrAlaIapSerHisAlaIapMetRellyIleAlaAlaAla	130
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Db	2835	CACATCTATGGAATTACTTTTGTATCTCTCAAGCATTTATGTATTTTCTATGCGGT	2894
Qy	491	GlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGluGlyMetPhe	510
Db	2895	TGTTTTCGATTTGGTGCAATCTCATTTGTGAATGGACATATGCGTTCACAGATGTTATT	2954

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Db	3075	CCTCTGATTGACGCTACAGTGAAGAGAGGGCGCTGAAGCGCTGATTAATTTGAAGGAAATATA	3134
Qy	571	GlupheArgGluValSerPhePheTyrProCysArgProAspValPheIleLeuArgGly	590
Db	3135	ACATTTAATGAAGTCGTGTTTCACTATCCACCCGAGCAACGTCGCAGCGTTCACGGG	3194

Qy 591 LeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSerGlyVCysGly 610
 3195 CTGAGCCTGAGGTTGAGAAAGGCCAGACACTAGCCCTGGTGGGCACAGTGGCTGTGGG 3254
 Db

QY 611 LysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGlyGlnValLeu 630
DB 3255 AGAGACCGGTGCTCAGCTCTCGGAGCGTCTACGACCCCTTGGCGGACAGTGTCTT 3314
QY 631 PheAspGlyValAspAlaLysGlnLeuAsnValGlnTyrLeuArgSerGlnLeuAlaLe 650
DB 3315 CTCGATGGTCAAGAACCAAGAACTCATGTCAGTGGCTCAGAGCTCACTCGGATC 3374
QY 651 ValProGlnGluProValLeuPheAsnGlySerLeuAlaGluAsnLeuAlaTyrGlyAsp 670
DB 3375 GTGTCTCAGAGCCATCTATTTGCTCAGCAGTTCGCGAGATATTTGCTTATGGAGAC 3434
QY 671 AsnSerArgValValProLeuAspGlnLeuLysGlnAlaAsnAlaAlaAsnLeuLeu 690
DB 3435 AACACCGGGTGTATCACAGATGAAATTCAGTGCAGCCCAAGAGTGCACACATACAT 3494
QY 691 SerPheLeuGluGlyLeuProGlnLysTyrAsnThrGlnValGlyLeuLysGlyAlaGln 710
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QY 731 IleLeuLeuLeuAspGlnAlaThrSerAlaLeuAspAsnAspSerGlnLysValValGln 750
DB 3615 ATCTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3674
QY 751 HisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHisArgLeuSer 770
DB 3675 GAAGCCCTCGACAAAGCCAGAGAGCCGACCTGCTGATTTGCTGCTGCTGCTGCTGCT 3734
QY 771 AlaIleGlnAsnAlaAspLeuLeuValValLeuHisAsnGlyLysLeuGlnGlyGln 790
DB 3735 ACCATCCAGATGACACTTATAGTGTGTTTCAGATGAGAGTGCAGAGGATGCTGCTG 3794
QY 791 ThrHisGlnGlnLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsnAlaGlnSer 810
DB 3795 AGCATCAGCAGCTGCTGCGACAGAAAGGACATCTATTTTCAATGCTCAGTGTCCAGCT 3854

RESULT 2

US-09-762-195-2
; Sequence 2, Application US/09762195
; Patent No. 6677319
; GENERAL INFORMATION:
; APPLICANT: Stremmel, Wolfgang
; TITLE OF INVENTION: Phosphatidylcholine as Medication with
; TITLE OF INVENTION: Protective Effect on Large Intestinal Mucosa
; FILE REFERENCE: 34691/208520
; CURRENT APPLICATION NUMBER: US/09/762,195
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: PCT/EP99/02426
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 198 35 526 2 DE
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 198 57 570.8 DE
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3924
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-762-195-2

Alignment Scores:
P-Id. No.: 1.74e-281 Length: 3924
Score: 2465.50 Matches: 478
Percent Similarity: 76.46% Conservative: 149
Best Local Similarity: 58.23% Mismatches: 182
Query Match: 60.44% Indels: 11
DB: 3 Gaps: 4

QY 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
DB 1395 ATTGATGGGAGGATATTAGGAACCTTTAATGTAACCTTATCTGAGGGAATCATTTGGTGTG 1454
QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
DB 1455 GTGAGTCAGGAGCCGGTCTGTTTTCACCACTTCTGTAATAATTTTGTATGGCCGT 1514
QY 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
DB 1515 GGAAATGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1574
QY 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
DB 1575 ATCATGAAATTTACCAAGAAATTTGACACCTTGTGGAGAGAGAGGGCCACGCTGAGT 1634
QY 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
DB 1635 GGTGGCAGAGCAGAGGATGCGCCATTCGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1694
QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGlnSerLysSerAlaValGlnAlaAla 121
DB 1695 CTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1754
QY 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141
DB 1755 CTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1814
QY 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
DB 1815 CGAAATGTCAGATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1874
QY 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuVal 175
DB 1875 AGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1934
QY 176 -----MetSerGlnAspIleLysAlaAspGluGlnMetGluSerMetThrTyr 192
DB 1935 AGCCAGATCCAGTCAGAGAAATTTGAATGATGATGATGATGATGATGATGATGATGAT 1994
QY 193 SerThrGluArgLysThrAsnSerLeuProLeuHisSerValLysSerIleLys 211
DB 1995 CCAATGGCTGGAATCTCGCTATTTAGGCATTTCTACTCAGAAAAACCTTTAAAAATTC 2054
QY 212 AspPheIleAspLysAla---GluGluSerThrGlnSerLysGluIleSerLeuProGlu 230
DB 2055 CAAATGTCAGAGAGCCTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2114
QY 231 ValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTyrPropheValValLeuGly 250
DB 2115 GTGTCTCTTCTGAAGGTCCTGAAACTGATATAAACAAGATGGCCCTACTTTGTCTGGGA 2174
QY 251 ThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePheAlaLys 270
DB 2175 ACATGATGCCATTTGCCAATGGGGGCTTCAGCCGCTATTTTCAGTCATATTTCTCAGAG 2234
QY 271 IleIleThrMetPheGlyAsnAsnAspLysThrThrLeuLysHisAspAlaGluIleTyr 290
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QY 291 SerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMetGlnGlyLeu 310
DB 2295 TCTTTGATTTCTTATTTCTGGGAATTTATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 2354
QY 311 PheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAlaPheLysAla 330
DB 2355 ACCTTTGGGAAAGCTGCGAGATCTCTCACCAGAGAGCTGCGGTCAATGGCTTTTAAAGCA 2414
QY 331 MetLeuTyrGlnAspIleAlaTyrPheAspGluLysGlnAsnSerThrGlyGlyLeuThr 350

Qy	711	LeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGlnLysProLys	730
Db	3555	CTCTCAGGAGGTCAAAACACAGAGATTGGCTATTGCCGAGCCCTCATATCAGACACCTCAA	3614
Qy	731	IleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLysValValGln	750
Db	3615	ATCCTCTGTGGATGAAGCTACATCAGCTCTGGATACTGAAAGTGAAGAAGTTGTCCAA	3674
Qy	751	HisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHisArgLeuSer	770
Db	3675	GAAGCCCTTGACAAAGCCAGAGAAGCGCACCTGCAATTGTGTGANTGCTCACCCGCTGTCC	3734
Qy	771	AlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLysGluGlnGly	790
Db	3735	ACCATCCGAATGCAGACTTAATAGTGGTGTTCAGAAATGGGAGAGTCAAAGGAGCATGGC	3794
Qy	791	ThrHisGlnGluLeuLeuArgAsnArgAspIleTyPhelLysLeuValAsnAlaGlnSer	810
Db	3795	ACGCATCAGCAGCTGTCTGGCACAGAAGGCACTATTTTTCAATGGTCAGTGTCCAGGCT	3854
RESULT 3			
US-09-672-810-1			
; Sequence 1: Application US/09672810			
; Patent No. 6617450			
; GENERAL INFORMATION:			
; APPLICANT: STOCKER, PENNY J.			
; APPLICANT: STEIMEL-CRESPI, DOROTHY T.			
; APPLICANT: CRESPI, CHARLES L.			
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF			
; FILE REFERENCE: G0307/7018			
; CURRENT APPLICATION NUMBER: US/09/672,810			
; CURRENT FILING DATE: 2000-09-28			
; PRIOR APPLICATION NUMBER: US 60/156,921			
; PRIOR FILING DATE: 1999-09-28			
; PRIOR APPLICATION NUMBER: US 60/158,818			
; PRIOR FILING DATE: 1999-10-12			
; NUMBER OF SEQ ID NOS: 18			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 1			
; LENGTH: 4186			
; TYPE: DNA			
; ORGANISM: Macaca fascicularis			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (100)...(3940)			
US-09-672-810-1			
Alignment Scores:			
Pred. No.:		1,53e-278	Length: 4186
Score:		2441.00	Matches: 465
Percent Similarity:		76.73%	Conservative: 168
Best Local Similarity:		56.36%	Mismatches: 174
Query Match:		59.84%	Indels: 18
DB:		4	Gaps: 5
US-09-873-409-2 (1-812) x US-09-672-810-1 (1-4186)			
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Db	1456	CTTGATGACAGAGATATTAGGACCATTAACGCTTAAGGTTTCTACGGGAATCATCGGTGTG	1515
Qy	22	ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyArgArg	41
Db	1516	GTGAGTCAGGAACCTGTATTGTTTGGCCACCATAGCTGTAAACAATTCCTATATGTCGT	1575
Qy	42	AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyArgPhe	61
Db	1576	GAAGATGTCACCATGATGATGATGAGAAAGCTGTCAGGAAGCCAAATGCTATGACTTT	1635
Qy	62	IleMetGluPheProAsnLysPheAsnThrLeuValGlyGlnLysGlyAlaGlnMetSer	81
Db	1636	ATCATGAACCTGCTCAGAAATTGACACCTGGTTGGAGAGAGAGGGGCCCACTGAGT	1695

QY 82 GlyGlyGlnArgIleAlaAlaAlaLeuValArgAsnProLysIleLeu 101
DB 1696 GGTGGGACAGACAGAGATCGCAATTCACGTGCGCTCGTTCGCAACCCCAAGATCCTC 1755
QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
DB 1756 CTGCTGGACAGGACCGTCAGCTTGGACACAGAAAGTGAAGCTGGTTCAGGTGGCT 1815
QY 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141
DB 1816 CTGGATAAGCCAGAAAGGTCGGACCACTTGTGATAGCTCATCGTTGTCTAGCGTT 1875
QY 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
DB 1876 CGTAATGCCGACGCTCATCGCTGCTTTCGATGATGGAGTCATTGTGGAGAAAGCAATCAT 1935
QY 162 AlaGluLeuMetAlaLysArgGlyLeuTyThrSerLeuValMetSerGlnAspIle--- 180
DB 1936 GATGAGCTCATGAAGAAGAAAGCACTTACTTCAAACTTGTCAATGTCAGACAGCA 1995
QY 181 -----LysLysAlaAspGlu-----GlnMetGluSerMetThr 191
DB 1996 AATGAATAATTAGAAATGAGCTGATGATCCAAAGTGAATGATACCTTGGAA 2055
QY 192 TyrSerThrGluArgLysThrAsnSerLeu-----ProLeuHisSerVal 206
DB 2056 ATGCTTCACATGATTCAGATCCAGTCTTAATGAAGAAAGATCCACTGTTAGGAGTGC 2115
QY 207 LysSerIleLysSerAspPheIleAspLysAlaGluSerThrGlnSerLysGluIle 226
DB 2116 CGTGGATCAACAGCCAA-----GACAGAAAGCTTAGTACCAAGAGCTCTGGATGA 2169
QY 227 SerLeuProGluValSerLeuLysIleLeuLysLeuAsnLysProGluTrpProPhe 246
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QY 247 ValValLeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIle 266
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QY 267 IlePheAlaLysIleIleThrMetPhe---GlyAsnAsnAspLysThrThrLeuLysHis 285
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QY 346 ThrGlyGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGly 365
DB 2530 ACTGGACCATGTACTACCGCTCGCCCAATGATGCTCTCAAGTTAAAGGGGTATAGGT 2589
QY 366 SerArgIleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSer 385
DB 2590 TCCAGGCTTCTGTAATATCCCGAATATATGCAAACTCTGGGACAGGAATAATATATATCC 2649
QY 386 PheIleTyThrGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaVal 405
DB 2650 TTAATCTATGTTGGCAACTGACATGTTTACTCTTAGCAATTGTACCCATTCATTCGCAAT 2709
QY 406 ThrGlyMetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeu 425
DB 2710 GCAGGAGTTGTAATGAAATGAAATGTTGCTGCAAGCACTGAAAGATGAAGAAAGCACTA 2769

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DB 2770 GAAGTGCTGGGAAGATCGCTACTGAAGCAATAAAAACTTCCGAACCTGTGTTCTTTTG 2829
QY 446 ThrArgGluLysAlaPheGluGlnMetTyThrGluGluMetLeuGlnThrGlnHisArgAsn 465
DB 2830 ACTCHGAGCGAAGAGTTTGAACATATGATCAGAGTTTGCAGGTACCATACAGAAAC 2889
QY 466 ThrSerLysLysAlaGlnIleIleGlySerCysTyThrAlaPheSerHisAlaPheIleTy 485
DB 2890 TCTTTGAGAAAGCACACATCTTTGGAATCAGCTTTTCTTTCACGCAGCAATGATGAT 2949
QY 486 PheAlaTyThrAlaAlaGlyPheArgPheGlyAlaTyLeuIleGlnAlaGlyArgMetThr 505
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QY 506 ProGluGlyMetPheIleValPheThrAlaIleAlaTyThrGlyAlaMetAlaIleGlyLys 525
DB 3010 TTTGAGGATGTTCTGTTAGTATTTTCACTGTTGCTTTGTTGGCCATGGCCGTGGGCAA 3069
QY 526 ThrLeuValLeuAlaProGluTySerLysAlaLysSerGlyAlaAlaHisLeuPheAla 545
DB 3070 CTCAGTTTCATTTGCTCTGACTATGCCAAAGCCAAAGTATCAGCAGCCACATCATCATG 3129
QY 546 LeuLeuGluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThr 565
DB 3130 ATCATTTGAATAAACCCCTTTGATTGACAGCTACACAGAGGCTTAAGCCGACACACA 3189
QY 566 CysGluGlyAsnLeuGluPheArgGluValSerPhePheTyThrProCysArgProAspVal 585
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QY 586 PheIleLeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGly 605
DB 3250 CCGTGCTTTCAGGGCTCAGCTGGAAGTGAAGAGGCCAGACGCTGGCTCTGTGGGC 3309
QY 606 SerSerGlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyThrAspProVal 625
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QY 626 GlnGlyGlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnTrpLeuArg 645
DB 3370 GCGGGGAAGTGCTGCTGACGGCAAGAAATAAGCAACTGAATGTTCACTGAGTGGCTCCA 3429
QY 646 SerGlnIleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsn 665
DB 3430 GCACACCTGGGCATCGTGTCCAGGAGGCCATCTCTGTTGACTGTCAGCATTAGTGAGA 3489
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QY 686 AlaAlaAsnIleHisSerPheIleGluGlyLeuProGluLysTyThrAsnThrGlnValGly 705
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DB 3610 GACAAAGGAACCTCAGCTCTCTGTTGGCCAGAAACAAACGATTCGCCATAGCTCTGTGCCCTT 3669
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DB 3670 GTTAGCAGCCCTCATTTTGTCTTGTGATGAAGCCACATCAGCTCTGGATACAGAAAT 3729
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QY 766 ThrHisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisArgGlyLys 785
DB 3790 GGTACCGCTGTCCACCATCCAGAAATGCGACTTAATAGTGTGTTTCAGAAATGCGACA 3849
QY 786 IleLysGluGlnGlyThrHisGlnLeuLeuArgAsnArgAspIleTyThrPheLysLeu 805

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Db 3910 GTCAAGTGCAGGCT 3924

RESULT 4
US-09-672-810-3
; Sequence 3, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STRIMEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4195
; TYPE: DNA
; ORGANISM: Macaca fascicularis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)...(3949)
US-09-672-810-3

Alignment Scores:
Pred. No.: 1,586-278 Length: 4195
Score: 2441.00 Matches: 465
Percent Similarity: 76.73% Conservative: 168
Best local Similarity: 56.36% Mismatches: 174
Query Match: 59.84% Indels: 18
DB: 4 Gaps: 5

US-09-873-409-2 (1-812) x US-09-672-810-3 (1-4195)
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Qy 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
Db 1525 GTGAGTCAGGAACCTGTATTTGTTTCCACCCAGATAGCTGAAACATTCGCTATGTCGT 1584
Qy 42 AspAspValThrAspGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 1585 GAAGATGTCACCATGGATGAGATTGAGAAAGCTGTCAAGGAAGCCCAATGCTATGACTTT 1644
Qy 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
Db 1645 ATCATGAAGTCCTCAGAAATTTGACACCTCGTGTGGAGAGAGGGGCCACCTGAGT 1704
Qy 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
Db 1705 GGTGGCAGAGAGCAGAGGATCGCAATTCAGCTGCCCTCGTGTGCAACCCCAAGATCCTC 1764
Qy 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
Db 1765 CTGCTGGACGAGGCGACCTGAGCTTGGACACAGAAAGTGAAGCAGGTGGTTCAGGTGGCT 1824
Qy 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141
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Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
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Db 1945 GATGAGCTCATGAAGAGAAAGGCAATTACTTCAAACTTGTCACAATGCAGACAGCAGGA 2004
Qy 181 -----LysLysAlaAspGlu-----GlnMetGluSerMetThr 191
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Qy 192 TyrSerThrGluArgLysThrAsnSerLeu-----ProLeuHisSerVal 206
Db 2065 ATGCTCTTCATCATCAATTCAGGATCCAGCTCTAATAAGAAAGATCCACTCGTAGGAGTGC 2124
Qy 207 LysSerIleLysSerAspPheIleAspLysAlaGluGluSerThrGlnSerLysGluIle 226
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Qy 446 ThrArgGluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsn 465
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Db 2083 CGTGATCACAAGCCCAAGACAGAAAGCTTGTAGTACCAAGAGAGGCTCTGGATGAAAGTATA 2142
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Qy 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
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Qy 328 PheLysAlaMetLeuThrGlnAspIleAlaTrpPheAspGluLysGluAsnSerThrGly 347
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Qy 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHis 427
Db 2683 GTTGTGTAATGAAATGCTGCTGCAAGCAAGCACTGAAAGATAAGAAAGAACTAGAAAGT 2742
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Qy 448 GluLysAlaPheGluGlnMetThrGluMetLeuGlnThrGlnHisArgAsnThrSer 467
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Qy 548 GluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGlu 567
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Qy 648 IleAlaIleValProGlnGluProValPheAsnCysSerIleAlaGluAsnIleAla 667
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Db 3463 TATGGAGACAACAGCGGCTGTGTTCACAGGAAGAGATTGTGAGGCGCAGCAAGAGGCGC 3522
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Qy 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValThrHis 767
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Qy 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 3763 CGCCTGTCCACCATCCAGATGCGAGACTTAATAGTGTGTTTTCAGAAATGCGCAGAGTCAAG 3822
Qy 788 GluGlyGlyThrHisGlnGluLeuLeuArgAsnArgAspIleThrPheLysLeuValAsn 807
Db 3823 GAGCATGGCAGCGATCAGCAGCTGCTGGCAGAAAGCGCATCTATTTTCAATGTCAGT 3882
Qy 808 AlaGlnSer 810
Db 3883 GTCCAGGCT 3891

RESULT 6
US-08-784-649A-1
; Sequence 1, Application US/08784649A
; Patent No. 5830697
; GENERAL INFORMATION:
; APPLICANT: Sikic, Branimir I
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
; TITLE OF INVENTION: CYCLOSPORIN MODULATION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/08/784,649A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sherwood, Pamela J
/ REGISTRATION NUMBER: Reg No. 5830697 36,677
/ REFERENCE/DOCKET NUMBER: 06037/007001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-322-5070
/ TELEFAX: 415-854-0875
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4264 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-784-649A-1

Alignment Scores:
Pred. No.: 6,39e-278 Length: 4264
Score: 2436.00 Matches: 466
Percent Similarity: 76.79% Conservative: 166
Best Local Similarity: 56.62% Mismatches: 177
Query Match: 59.72% Indels: 14
DB: 2 Gaps: 4

US-09-873-409-2 (1-812) x US-08-784-649A-1 (1-4264)
QY 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
DB 1495 GTTGATGGACAGGATATTAGGACCAATAAATTAAGGTTTCTACGGGAATCATTCGTGTG 1554
QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
DB 1555 GTGAGTCAGGAACCTGATGTTGTCACACAGATAGCTGTCAAGGAAGCAATTCGCTATGCGCT 1614
QY 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
DB 1615 GAAATGTCACCATGATGAGATGAGAAAGCTGTCAAGGAAGCAATTCGCTATGACATT 1674
QY 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
DB 1675 ATCATGAATGCTCCTCATAAATTTGACACCCCTGGTTGGAGAGAGAGGGCCAGTTGAGT 1734
QY 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
DB 1735 CGTGGACAGACAGAGAGATCGCCATTGACGTGCGCTGTTGCGAACCCCAAGATCCTC 1794
QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAla 121
DB 1795 CTGCTGGATGAGCCACGTCAGCTTGGACACAGAAAGCGAAGCAGTGGTTCAGGTGCT 1854
QY 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaAlaHisArgLeuSerThrIle 141
DB 1855 CTGGATAGCCAGAAAGGTCGACACCATTTGTATGATGCTCCTGTTGTCTACAGTT 1914
QY 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
DB 1915 CGTAATGCTGACGTCATCCTGTTTCGATGATGAGTCAATTTGGAGAAAGCAATCAT 1974
QY 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGln 178
DB 1975 GATGAACATCATGAAGAGAAAGGCAATTTACTTCAAACTGTGTCACATGACAGACACAGGA 2034
QY 179 -----AspIleLysLysAlaAspGluGlnMetGluSerMetThrTyrSerThrGlu 195
DB 2035 AATGAAGTTGAATTAGAAATGACGCTGATGATGATCCAAAGTGAATTTGATTCCTTGGAA 2094
QY 196 ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209
DB 2095 ATGTCTTCAATGATTCAAGATCCAGTCTAATAAGAAAAAGATCAACTCGTAGGAGTGTCT 2154

210 Lys---SerAspPheIleAspLysAlaGluGluSerThrGlnSerLysGluLeuSerLeu 228
2155 COTGGATCACAGGCCAAGACAGAAAGCTTAGTACCAAGAGGCTCTCGATGAAGATATA 2214
QY 229 ProGluValSerLeuLysIleLeuLysLeuAsnLysProGluTyrProPheValVal 248
2215 COTCAGTTTCTTTTGGAGGATATAGCTTAATTAATTAAGTAACTGATGCTTATTTGTT 2274
QY 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
2275 GTTGGTGATTTTGTGCCATATATAATGGAGCGCTGCAACAGCAGCATTTTGCATAATATT 2334
QY 269 AlaLysIleIleThrMetPheGlyAsn---AsnAspLysThrThrLeuLysHisAspAla 287
2335 TCAGAATATAGGGGTTTTTACAGAATTTCTGAAACAAACAGCAGAGATAGT 2394
QY 288 GluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMet 307
2395 AACTTGTCTTCACTATTGTTCTAGCCCTTGGAAATATTCTTTTATTACATTTTTCCTT 2454
QY 308 GlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAla 327
2455 CAGGGTTTTCATATTGGCAAGAGCTGGAGAGATCTCTACCAAGCGGCTCCGATACATGTT 2514
QY 328 PheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAspGluLysGluAsnSerThrGly 347
2515 TTCGATCCATGCTCAGACAGAGTGTGAGTTGGTTTGATGACCTTAATAAACACCACTGGA 2574
QY 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
2575 GCATTGACTACAGGCTGCGCAATGATGCTGCTCAAGTTAAAGGGGCTATAGTTTCCAGG 2634
QY 368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
2635 CTGCTGTAATTTACCAGATATATAGCAATCTTGGGACAGGAATTAATTAATTCCTTCATC 2694
QY 388 TyrGlyTyrGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGly 407
2695 TATGTTGGCAACTAACACTGTTACTCTTAGCAATTTGATCCCATCATCTTGCATACAGCA 2754
QY 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLysHis 427
2755 GTTGTGGAATGAAATGTTGCTGAGACAGCATGGAAGATAGAAGAACTAGAAAGT 2814
QY 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArg 447
2815 CTTGGGAAGATCGCTACTGGAAGCAATAGAAAACCTTCGAAACCGTTGTTCTTTGACTCAG 2874
QY 448 GluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
2875 GAGCAGAAGTTTGAACATATGATGCTCAGAGTTTGCAGGTACCATACAGAAACTCTTTG 2934
QY 468 LysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAla 487
2935 AGGAAGCAGACATCTTTGGAAATTTACATTTCTTCCACCGGCAATGATGATGATTTTCC 2994
QY 488 TyrAlaAlaGlyPheArgPheGlyValTyrLeuIleGlnAlaGlyArgMetThrProGlu 507
2995 TATGCTGATGTTTCGCTTTGGAGCGCTACTTGTGGGCACATAAACAATCATGAGTTTGAG 3054
QY 508 GlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeu 527
3055 GATGTTCTGTTAGTATTTTTCAGCTGTTGCTTGTGGTCCATGCGCGGCGGCAAGTCACT 3114
QY 528 ValLeuAlaProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547
3115 TCATTTGCTCTGACTATGTCAAAGCCAAATATATCAGCAGGCCCATCATCATGATCATTT 3174
QY 548 GluLysLysProAsnIleAspSerArgSerGlnGlnGlyLysLysProAspThrCysGlu 567
3175 GAAAAAACCCCTTTGATTGACAGCTACAGCAGGAGGCTTAATGCGCAACACATTTGAA 3234
QY 568 GlyAsnLeuGluPheArgGluValSerPhePheTyrProCysArgProAspValPheIle 587
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Db 3235 GGAATGTCACATTTGGTGAAGTGTATTCACATCCACCGACCGACATCCAGTG 3294
Qy LeuArgGlyLeuSerLeuSerIleGluArgGlyThrValAlaPheValGlySerSer 607
Db 3295 CTTGAGGAGTGGAGTGGAGTGAAGAGGCGCAGACGCTGCTCTGGTGGCAGCAGT 3354
Qy GlyCysGlyValSerThrSerValGlnLeuGlnArgLeuValProValGlnGly 627
Db 3355 GCGTGTGGAGAGACACAGTGTCTCCAGTCTCTGGAGCGGTCTACAGCCCTTGGCAGG 3414
Qy GlnValLeuPheAspGlyValAspAlaValGluLeuValGlnTrpLeuArgSerGln 647
Db 3415 AAGTGTCTGTGATGTCAGCAAGAAATAAGCGCATGAATGTTTCAGTGGCTCCGAGCAC 3474
Qy IleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAla 667
Db 3475 CTGGGCACTGTGTCAGGAGCCCTCTCTGTTGACTGACGCHTGTCTGAGACATGTC 3534
Qy TyrGlyAspAsnSerArgValValProLeuAspGluIleLeuValGluAlaAsnAla 687
Db 3535 TATGAGACACACCGCGGTGTGTCTACAGAGAGATTTGTGAGGCGCAGCAAGGAGGCC 3594
Qy AsnIleHisSerPheIleGluGlyLeuProGluLysThrAsnThrGlnValGlyLeuLys 707
Db 3595 AACATACATGCTTCATCGAGTCTACTGCTCTTAATAATATAGCACTAAGTAGGAGCAAA 3654
Qy GlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGln 727
Db 3655 GGAATCAGCTCTCTGTGGTGGCCAGAAACAGCGCATGTCCTGTCCTTGTAGA 3714
Qy LysProLysIleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLys 747
Db 3715 CAGCTCATATTTTGTGTTGATGAGAGCCACGTCAGCTCTGATACAGAAAGTGAAG 3774
Qy ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHis 767
Db 3775 GTTGTGCAAGAGCCCTGGCAAGAGCCAGAGAGCGCCACCTGCTGATGTTGCTCAC 3834
Qy ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 3835 CGCTGTGTCACCATCCAGATGCGAGACTTAATAGTGGTGTTCAGATGCGCAGATCAAG 3894
Qy GluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleValPheLysLeuValAsn 807
Db 3895 GAGCATGGCAGCATCAGCAGTCTCTGCGCAGAGAGGCGATCTATTTTCAATGGTCA 3954
Qy AlaGlnSer 810
Db 3955 GTCCAGGCT 3963

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RESULT 7

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US-08-784-649A-5
; Sequence 5, Application US/08784649A
; Patent No. 5830697
; GENERAL INFORMATION:
; APPLICANT: Chen, Gang
; APPLICANT: Sikic, Branimir I
; TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
; TITLE OF INVENTION: CYCLOSPORIN MODULATION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-354-0875
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-784-649A-5

Alignment Scores:
Pred. No.: 6,39e-278 Length: 4264
Score: 2436.00 Matches: 466
Percent Similarity: 76.79% Conservative: 166
Best Local Similarity: 56.62% Mismatches: 177
Query Match: 59.72% Indels: 14
Gaps: 4

US-09-873-409-2 (1-812) x US-08-784-649A-5 (1-4264)
Qy 2 ValAspGluAsnAspIleArgAlaLeuAsnValAlaGHisTyrArgAspHisIleGlyVal 21
Db 1495 GTTGATGGACAGATATTAGGACCATTAATTAAGTTTCTACGGGAATCATTTGGTGG 1554
Qy 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
Db 1555 GTGAGTCAGAACCTGTATTGTTTCCACCATGATAGCTGAAACATTCGCTATGGCCGT 1614
Qy 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 1615 GAAATGTCTCATGTGATGATGATGAGAAAGCTGTCAAGAAAGCCATGCTTATGACTTT 1674
Qy 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyValAlaGlnMetSer 81
Db 1675 ATCATGAAATCCCTCATATAATTTGCACACCTGTTGGAGAGAGAGGGGCCAGTTGAGT 1734
Qy 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
Db 1735 GGTGGGCAAGACAGAGGATCGCCATTCACGTGCTGCTGTTCCGCAACCCCAAGATCTTC 1794
Qy 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
Db 1795 CTGCTGATGAGCCACCGTCAGCTTGGACACAGAAAGCGAGCAGTGGTTTCAGGTGGCT 1854
Qy 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141
Db 1855 CTGGATAAGCCAGAAAGGTGGACCCATTTGATAGTACCTCATCGTTTGTCTACAGTT 1914
Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
Db 1915 CGTAATGCTGACGTCACTCATCGCTGTTTCGATGATGATGATGATGATGATGATGAT 1974
Qy 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGln----- 178
Db 1975 GATGAACCTCATGAAGAGAGAGAGCATTTACTTCAAACTTGTCAATGACAGACAGAGCA 2034
Qy 179 -----AspIleLysLysAlaAspGluGlnMetGluSerMetThrTyrSerThrGlu 195
Db 2035 ATGGAAGCTTGAATAGAAATGACGTGATGATGATGATGATGATGATGATGATGATGAT 2094
Qy 196 ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209
Db 2095 ATGCTCTTCAATGATTCAGATCCAGTCTAATAAGAAAGAAAGTCAACTCGTAGGAGTGT 2154

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QY 568 GlyAsnLeuGluPheAsgGluValSerPhePheTyrProCysAArgProAspValPheIle 587
DB 3235 GGAATGTCACATTTGGTGAAGTTGTATTAACCTATCCACCCGACCCGACATCCAGTG 3294
QY 588 LeuArgGlyLeuSerLeuSerIleGluArgGlyThrValAlaPheValIleGlySerSer 607
DB 3295 CTTGAGGACTGAGCTGGAGTGAAGAGGCGGACGCTGGCTCTGGTGGGACGAGT 3354
QY 608 GlyCysGlyLeuSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGly 627
DB 3355 GCGTGTGGAGAGACACAGTGTCTGAGTCTCTGGAGCGTCTTACGACCCCTTGGCAGG 3414
QY 628 GlnValLeuPheAspGlyValAlaAlaGlyLeuLeuValGlnTrpLeuArgSerGln 647
DB 3415 AAAGTCTGCTGTATGGCAAGAAATAAAGGACTGATGTTCAGTGTCTGCGACACAC 3474
QY 668 IleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAla 667
DB 3475 CTGGCATCGTGTCCAGAGCCCATCTCTGTGACTGCACATTCCTGAGAACATTGCC 3534
QY 668 TyrGlyAspAsnSerArgValProLeuAspGlyLeuIleLysGluAlaAlaAsnAla 687
DB 3535 TATGGAGACACAGCCGGTGTGTACAGAGAGATTTGTGAGGCGAGCAAGAGGCC 3594
QY 688 AsnIleHisSerPheIleGluGlyLeuProGlyLysTyrAsnThrGlnValGlyLeuLys 707
DB 3595 AACATACATGCTTTCATGAGTCACTGCTTAATAATATAGCATTAAGTAGGAGACAAA 3654
QY 708 GlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuGln 727
DB 3655 GGAAGTCTCTCTGTTGGCCAGAACACGATTCGCTAGCTCTGCTGCTTTGTAGA 3714
QY 728 LysProLysIleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnSerGlyLys 747
DB 3715 CAGCTCATATTTTGTCTTTGATGAAGCCAGCTGCTGATGATACAGAAAGTGAAG 3774
QY 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValThrHis 767
DB 3775 GTTGTCCAGAGCCCTGGACAAAGCCAGAGAGCCGACCTGCATTTGTGTTGCTCAG 3834
QY 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
DB 3835 GCGCTGTCCACCATCCAGATGACAGCTTAATAGTGTGTTCAGAAATGGCAGAGTCAAG 3894
QY 788 GluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsn 807
DB 3895 GAGCATGGCAGCATCAGCAGCTGTGGCAGAAAGGCACTATTTTCAATGGTCACT 3954
QY 808 AlaGlnSer 810
DB 3955 GTCCAGGCT 3963
RESULT 8
US-08-181-471-2
; Sequence 2, Application US/08181471
; Patent No. 5641508
; GENERAL INFORMATION:
; APPLICANT: Li, Lingna
; APPELLANT: Lishko, Valeryi K.
; TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
; COMPOSITIONS TO HAIR FOLLICLES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas Pitting
; STREET: 12526 High Bluff Drive, Suite 300
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

QY 210 Lys---SerAspPheIleAspLysAlaGluGluSerThrGlnSerLysGluIleSerLeu 226
DB 2155 CGTGGATCAAGCCCAAGACAGAGAGCTTAGTACCAAGAGGCTCTGGATGAAGTATA 2214
QY 229 ProGluValSerLeuLysIleLeuLysLeuAsnLysProGluTrpProPheValVal 248
DB 2215 CTTCCAGTTCTCTTTTGGAGGATTAAGAAGCTAAATTTAACTCAATGGCTTATTTGTT 2274
QY 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
DB 2275 GTTGGTGTATTTTGGCCATTATAAGGAGGCTGCAACCGACTTTGCAATAATATT 2334
QY 269 AlaLysIleIleThrMetPheGlyAsn---AsnAspLysThrThrLeuLysHisAspAla 287
DB 2335 TCAAGATATATAGGGGTTTTTCAAGATTTGATGATCTCTGAAACAAACGACAGAAATAGT 2394
QY 288 GluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMet 307
DB 2395 AACTGTTTCTACTATTTCTAGCCCTTGAATTTATTTCTTTATACATTTTCTCT 2454
QY 308 GlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAla 327
DB 2455 CAGGGTTTCAATTTGGCAAGCTGGAGAGATCTTCCACCAAGGGCTCGATACATGTT 2514
QY 328 PheLysAlaMetLeuTyrGlnAspIleAlaTrpPheAspGlyLysGluAsnSerThrGly 347
DB 2515 TTCCGATCCATGCTCAGACAGGATGTGAGTGTGTTGATGACCCCTTAAACACACCACTGGA 2574
QY 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
DB 2575 GCATTGACTACAGGCTCCGCCAATGCTGCTCAAGTTTAAAGGGCTATAGTTCCAG 2634
QY 368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
DB 2635 CTTGCTGTAATACCCAGAAATATAGCAATCTTGGACAGGAATAATATATCTTCTATC 2694
QY 388 TyrGlyTyrGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGly 407
DB 2695 TATGGTGGCAACTAACACTGTACTCTTAGCAATTTGATCCCATCATTTGCAATAGCAGA 2754
QY 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHis 427
DB 2755 GTTGTGTAATGAATGTTGCTGGACAGCACTGCAAGATAGAAAGAACTAGAGGT 2814
QY 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArg 447
DB 2815 GCTGGAGAGATCGCTACTGAGCAATAGAAACTTCCGAAACCGTTGTTCTTTGACTCAG 2874
QY 448 GluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
DB 2875 GAGCAGAGCTTTGAACATATGATGCTCAGAGTTTGCAGGTACCATACAGAACTCTTTG 2934
QY 468 LysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAla 487
DB 2935 AGGAAAGCACACATCTTTGGAATTAATTTCTTCCACCCAGGCAATGATGATTTTCTCC 2994
QY 488 TyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGlu 507
DB 2995 TATGCTGGATGTTCCGGTTTGGAGCTTACTTGGTGGCAGCATAAAGTATGAGCTTTGAG 3054
QY 508 GlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeu 527
DB 3055 GATGTTCTCTAGTATTTTCACTGTGTCTTTGTTGGCCATGCGCGCTGGGCAAGTCACT 3114
QY 528 ValLeuAlaProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547
DB 3115 TCATTGCTCTGACTATGCCAAAGCCAAATATATCAGCAGCCCAATCATCATCATCAT 3174
QY 548 GluLysLysProAsnIleAspSerArgSerGlnGlyLysLysProAspThrCysGlu 567
DB 3175 GAAAAACCCCTTTGATTGACAGCTACAGCAGGAGGCGCTAATGCCAACACATTTGAA 3234

CURRENT APPLICATION DATA: US/08/181.471
 APPLICATION NUMBER: 424
 FILING DATE: 13-JAN-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/041,553
 FILING DATE: 02-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: ANT0029P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-792-3680
 TELEFAX: 619-792-8477
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4646 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 425..4267
 US-08-181-471-2

Alignment Scores:
 Pred. No.: 7,436-278 Length: 4646
 Score: 2436.00 Matches: 466
 Percent Similarity: 76.73% Conservative: 166
 Best Local Similarity: 56.62% Mismatches: 177
 Query Match: 59.72% Indels: 14
 DB: 1 Gaps: 4

US-09-873-409-2 (1-812) x US-08-181-471-2 (1-4646)

QY 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
 DB 1781 GTTGATGACAGCATATTAGGACCAATAAATGTAAGGTTTCTACGGGAAATCATTTGGTGTG 1840
 QY 22 ValSerGlnGluProValLeuPheGlyThrIleSerAsnAspIleLysTyrGlyArg 41
 DB 1841 GTGAGTCAGAACCTGTATTGTTGCCACCATGATGCTGGAACATTCGCTATGGCGT 1900
 QY 42 AspAspValThrAspGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
 DB 1901 GAAATGTCCACATGATGAGTTCAGAAAGCTGTCAAGGAAGCAATGCTATGACTTT 1960
 QY 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyValAlaGlnMetSer 81
 DB 1961 ATCATGAACCTCCATATAATTTGACACCTTGGTTGGAGAGAGGGGCCAGTTGAGT 2020
 QY 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
 DB 2021 GGTGGGCAAGACAGAGGATGCCATTCACGTGCCCTGTTGGCAACCCCAAGATCCTC 2080
 QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
 DB 2081 CTGCTGGATGAGCCACGTCAGCTTGGACACAGAAAGCAAGAGTGGTTCAGTGGCT 2140
 QY 122 LeuGluLysAlaSerLysGlyArgThrIleValValAlaHisArgLeuSerThrIle 141
 DB 2141 CTGGATAAGCCAGAAAGTCCGACCATTCATTTGATAGTCTATCGTTTGTCTACAGTT 2200
 QY 142 ArgSerAlaAspLeuValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
 DB 2201 CGTAATGCTGAGTCATCGCTCGTTTCGATGATGAGTCAITTTGGAGAAAGGAATCAT 2260
 QY 162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGln----- 178

2261 GATGAACCTCATGAAAGAGAAAGGCATTTTACTTTCAAACTTTGTACAAATGCAGACAGCAGGA 2320
 QY 179 -----AspIleLysLysAlaAspGluGlnMetGluSerMetThrTyrSerThrGlu 195
 DB 2321 AATGAAGTTGAATTAGAAATGAGCTGATGAATCCAAAGTGAATTAATGATGCTTGGAA 2380
 QY 196 ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209
 DB 2381 ATGCTCTCAATGATTCAAGATCCACTTAATAAGAAAAAGATCAAACTCGTAGAGTGT 2440
 QY 210 Lys---SerAspPheIleAspLysAlaGluGluSerThrGlnSerLysGluIleSerLeu 228
 DB 2441 CGTGGATCACAAAGCCCAAGACAAAGCTTAGTACCAAGAGGCTCTGATGAAGATATA 2500
 QY 229 ProGluValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTrpProPheValVal 248
 DB 2501 CTTCCAGTTTCTTTTGGAGGATTATGAAGCTAAATTTAACTGAATGGCTTATTTTGT 2560
 QY 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
 DB 2561 GTTGGTGTATTTTGTGCCATTATAAATGGAGGCTCTCAACCACTTTCGAATATATTT 2620
 QY 269 AlaLysIleIleThrMetPheGlyAsn---AsnAspLysThrThrLeuLysHisAspAla 287
 DB 2621 TCAAGATTATAGGGCTTTTACAGAAATGATGATCCTGAAACAAACAGACAGATAGT 2680
 QY 288 GluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMet 307
 DB 2681 AACTGTGTTTCACTATTGTTTCTAGCCCTTGGAAATTTCTTTTATTATCATTTTTCCT 2740
 QY 308 GlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAla 327
 DB 2741 CAGGTTTTCATTTGGCAAGCTGGAGAGATCTCACCAGCGGCTCCGATACATGGTT 2800
 QY 328 PheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAspGluLysGluAsnSerThrGly 347
 DB 2801 TTCGATCCATGCTCAGACAGGATGTGAGTTGTTGATGACCTTAAACACACCTGGA 2860
 QY 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
 DB 2861 GCATTGATCAGGCTCCGCAATGATGCTGCTCAGTTAAAGGGCTATAGTTCAGG 2920
 QY 368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
 DB 2921 CTTGCTGTAATCCCAAGATATAGCAAAATCTTGGACAGCAATAATATATATCTTCATC 2980
 QY 388 TyrGlyTyrGluMetThrPheLeuIleSerIleAlaProValLeuAlaValThrGly 407
 DB 2981 TAGGTTTGGCACTTAACACTGTTTACTCTTACCAATTTGTCCTCATCTGCAATAGCAGGA 3040
 QY 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHis 427
 DB 3041 GTTGTGAAATGAAATGTTTGTCTGGACAGCACTGAAGATAGAAGAAAGACTAGAAGGT 3100
 QY 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerIleThrArg 447
 DB 3101 GCTGGGAAGATCGCTACTGAAAGCAATAGAAAACTTCGGAACCGTTGTTCTTTGACTCAG 3160
 QY 448 GluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
 DB 3161 GAGCAGAGTTTGAACATATGATGCTCAGAGTTTGCAGGTACCATCAGAAACTCTTTG 3220
 QY 468 LysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAla 487
 DB 3221 AGAAAGCACACATCTTTGGAATTACATTTTCTTCCACCAGCAATGATGATTTTTC 3280
 QY 488 TyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGlu 507
 DB 3281 TATGCTGAGTTTCCGGTTTGGAGCTTACTTGGTGCAACATAAATCATGAGCTTTGAG 3340
 QY 508 GlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeu 527
 DB 3341 GATGTTCTGTAGTATTTTTCAGCTGTGTTGTTGGTCCATGTCCTGGGCGGCAAGTCAGT 3400

QY 528 ValLeuAlaProGluTyrSerIysAlaIysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547
Db 3401 TCATTGTCTCTGACTATGCCAAAGCAAAATATCAGCAGCCACATCATCATGATCAT 3460
QY 548 GluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGlu 567
Db 3461 GAAAAACCCCTTGTATTGACAGCTACACAGCAGAGGCTAATGCCGACACATGGAA 3520
QY 568 GlyAsnLeuGluPheArgGluValSerPhePheTyrProCysArgProAspValPheIle 587
Db 3521 GGAATGTTCACATTTGGTGAAGTTGATTCAACTATCCACCCGACCGGACATCCAGTG 3580
QY 588 LeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSer 607
Db 3581 CTTCAGGAGTGTGCTGAGGTGAGAGAGGCGCAGACCTGCTCTGTGGGACAGCT 3640
QY 608 GlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGly 627
Db 3641 GGCTGTGGGAGAGACACAGTGTGTCAGCTCTCTGGAGCGGTTCATGACCCCTTGGCAGGG 3700
QY 628 GlnValLeuPheAspGlyValAspAlaIysGluLeuAsnValGlnTyrLeuArgSerGln 547
Db 3701 AAGTGTCTGTGATGCGAAGAAATGAAAGCGACTGATGTTGAGTGGCTCCGAGCACAC 3760
QY 648 IleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAla 667
Db 3761 CTGGGATGTGTCTCCAGAGCCATCTCTGTGACTGCGAGCATGCTGAGAACATTTGCC 3820
QY 668 TyrGlyAspAsnSerArgValValProLeuAspGluIleLysGluAlaIleAlaAla 687
Db 3821 TATGGAGACAACACCGCGGTGTGTACAGAGAGAGATGTCGAGGGCAGCAAGGAGGCC 3880
QY 688 AsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLys 707
Db 3881 AACATATCTCTTCATCGAGTCACTGCTTAATATATAGCACTAAAGTAGGAGCAAA 3940
QY 708 GlyAlaGlnLeuSerGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuGln 727
Db 3941 GGAATCAGCTCTCTGTGGCCAGAAACAGCATTTGCCATAGCTGTGCTTGTGTTAGA 4000
QY 728 LysProLysIleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGlyLys 747
Db 4001 CAGCCTCATATTTGCTTTTGGATGAAGCCACGCTGATGATACAGAAAGTGAAGAG 4060
QY 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHis 767
Db 4061 GTTGTCCAGAGCCCTGGACAAAGCCAGAGAGGCGGACCTGCATTTGATGTGCTAC 4120
QY 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 4121 CGCCTGTCCACCATCCAGATGCGAGACTTAATAGTGTGTTTCAGATGCGCAGAGTCAAG 4180
QY 788 GlnGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsn 807
Db 4181 GAGATGCGACGATCAGCAGCTGCTGGCAGAAAGGCGATCTATTTTCATGTGCTCAGT 4240
QY 808 AlaGlnSer 810
Db 4241 GTCCAGGCT 4249

RESULT 9
US-09-023-655-1167
; Sequence 1167, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1167:
SEQUENCE CHARACTERISTICS:
LENGTH: 4646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g187468
US-09-023-655-1167

Alignment Scores:
Pred. No.: 7,436-278 Length: 4646
Score: 2436.00 Matches: 466
Percent Similarity: 76.79% Conservative: 166
Best Local Similarity: 56.62% Mismatches: 177
Query Match: 59.72% Indels: 14
DB: 4 Gaps: 4
US-09-873-409-2 (1-812) x US-09-023-655-1167 (1-4646)
QY 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
Db 1781 GTTGATGGACAGGATATTAGGACCAATAATGTAAGTTTCTAOGGAAATCATTCGTGTG 1840
QY 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleIysTyrGlyArg 41
Db 1841 GTGAGTCAAGAACCTGTATTGTTTCCACCACGATAGCTGAAACATTCGCTATGCGCGT 1900
QY 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 1901 GAAATGTTCATGTGATGAGATTGAAAGCTGTCAAGGAAGCCATGCTATGACTTT 1960
QY 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
Db 1961 ATCATGAAATTCCTATAAATTCACACCTCTGTTGGAGAGAGAGGGGCCCATGTTGACT 2020
QY 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
Db 2021 GTTGGGAGAGACAGAGGATCCCATTCACGTGCTGCTGTTGGTGGCAACCCCAAGATCTTC 2080
QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
Db 2081 CTGCTGGATGAGGCCCGTCAGCTTGGACACAGAAAGGAGACAGTGGTTCAGGTGGCT 2140
QY 122 LeuGluLysAlaSerLysGlyArgThrThrIleValValAlaHisArgLeuSerThrIle 141

Db 2141 CTGGATAAGCCGAGAAAGGTCGGACCAACCATTTGTGATAGCTCATCGTTTGTCTACAGTT 2200
Qy 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyValAlaHis 161
Db 2201 CGTAATGCTGACGTCATCGCTGGTTTCGATGATGAGTCAATGTGTGGAGAAAGGAATCAT 2260
Qy 162 AlaGluLeuMetAlaLysArgGlyLeuTyrrSerLeuValMetSerGln----- 178
Db 2261 GATGAACATCATGAAGAGAGAGGATTTTACTTCAAACTGTGCAAAATGCCAGACGACGGA 2320
Qy 179 -----AspIleLysLysAlaAspGluGlnMetGluSerMetThrTyrrSerThrGlu 195
Db 2321 AATGAAGTTGAATAGABAAATGCAGCTGATGAATCCAAAGTGAATGTATGCTCTGGA 2380
Qy 196 ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209
Db 2381 ATGCTCTTCAAAATGATTCAGATCCAGTCTAATAAGAAAAAGATCAACTCGTAGAGTGTG 2440
Qy 210 Lys---SerAspPheIleAspLysAlaGluGlnSerThrGlnSerLysGluLysSerLeu 228
Db 2441 CGTGGATCACAAGCCCAAGACAGAAAGCTTAGTACCAAGAGAGGCTCTGGATGAAGTATA 2500
Qy 229 ProGluValSerLeuLysIleLysLysLeuAsnLysProGluTrrProPheValVal 248
Db 2501 CCTCAGTTTCTTTTGGAGGATTATGAAGCTAAATTTAACTGAATGGCTTATTTTGT 2560
Qy 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
Db 2561 GTTGGTGTATTTTGGCCATTATTAATGAGGCTCTGCAACCGCATTTTGCATATATATT 2628
Qy 269 AlaLysIleIleThrMetPheGlyAsn---AsnAspLysThrThrLeuLysHisAspAla 287
Db 2621 TCMAAGATTATAGGGTTTTCACAGAAATTCATGATCTCTGAACACAAACGACAGATAGT 2680
Qy 288 GluIleTyrrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyrrPheMet 307
Db 2681 AACTTGTHTTCACTAATTTGTTCCCTTGGATTTATTTCTTTTATATACATTTTCTCT 2740
Qy 308 GlnGlyLeuPheTyrrGlyArgAlaGlyIleLeuThrMetArgLeuArgHisLeuAla 327
Db 2741 CAGGGTTTCACATTTGGCAAGCTGAGAGATCTCTACCAAGCGCTCCGATACATCGTT 2800
Qy 328 PheLysAlaMetLeuTyrrGlnAspIleAlaTrpPheAspGluLysGluAsnSerThrGly 347
Db 2801 TTCCGATCCATGCTCAGACGAGATGAGTGTGTTGATGATCCCTTAAACACCACTGGA 2860
Qy 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
Db 2861 GCATTGATCACCAGCTCGCCAAATGATGCTCTCAAGTTAAAGGGCTATAGTTCACGG 2920
Qy 368 IleGlyValLeuThrGlnAspAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
Db 2921 CTGTCTGTAATTAACCAATATAGCAAAATCTTGGGACAGGAATAATATATATCTTTCATC 2980
Qy 388 TyrrGlyTrpGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGly 407
Db 2981 TATGTTGGCAACTMACCTGTACTCTAGCANTTGTACCATTTGACCATTTGCATAGCAGGA 3040
Qy 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnLeuLysHis 427
Db 3041 GTTGTGTAATGCAAAATCTTCTCGCAAGCACTGAAAGATAAGAAAGAACTAGAAGGT 3100
Qy 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArg 447
Db 3101 CTGGGAGATGCTGCTACTGAAGCAATAGAAACTTCCGACCGTGTGTTTCTTGTACCTCAG 3160
Qy 448 GluLysAlaPheGluGlnMetTyrrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
Db 3161 GAGCAGAAAGTTTGAACATATGATGCTCAGAGTTTGCAGGTACCATCAGAAACTCTTTG 3220
Qy 468 LysLysAlaGlnIleIleGlySerCysTyrrAlaPheSerHisAlaPheIleTyrrPheAla 487
Db 3221 AGGAAAGCACACATCTTTTGGAAATACATTTTCTCTTCCCTTCCACCCAGGCAATGATGATTTTTC 3280

Qy 488 TyrAlaAlaGlyPheArgPheGlyAlaTyrrLeuIleGlnAlaGlyArgMetThrProGlu 507
Db 3281 TATGCTGGATGTTTCCGGTTTGGAGCTACTTGGTGGCACAATAAATCATGAGCTTTGAG 3340
Qy 508 GlyMetPheIleValPheThrAlaIleAlaTyrrGlyAlaMetAlaIleGlyLysThrLeu 527
Db 3341 GATGTTCTGTAGTATTTTTCAGCTGTGTCTTTTGGTGCATGCGCTGGGCGAAGTCAGT 3400
Qy 528 ValLeuAlaProGluTyrrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547
Db 3401 TCATTGCTCTGACTATGTCAAAGCCAAATAATATCAGCAGCCACATCATCATGATCAT 3460
Qy 548 GluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGlu 567
Db 3461 GAAAAAACCCCTTTGATTGACAGCTACAGCAGGAAGGCTTAATGCCGACACATTTGGA 3520
Qy 568 GlyAsnLeuGluPheArgGluValSerPheTyrrProCysArgProAspValPheIle 587
Db 3521 GGAATGTCACATTTGCTGAAGTTGATTCAACTATCCCAACCCGACCGGACATCCAGTG 3580
Qy 588 LeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSer 607
Db 3581 CTTCAAGGACTGAGCTGAGGCTGAAGAGGCGGACAGCTGCTGCTCTGGTGGGAGCAGT 3640
Qy 608 GlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyrrAspProValGlnGly 627
Db 3641 GGTGTGGGAGAGACACAGTGTCTCAGCTCTCTGGAGCGGTCTTACACCCCTTTGGCAGGG 3700
Qy 628 GlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValGlnTrpLeuArgSerGln 647
Db 3701 AAAGTGTCTGTTGATGCCAAAGAAATPAAAGCGACCTGAATGTTTCAAGTGGTCCGAGCAC 3760
Qy 648 IleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAla 667
Db 3761 CTGGGATCTGTCTCCAGGAGCCATCTCTGTTGACTGTCAGCATTCCTGAGAACATTTGCC 3820
Qy 668 TyrGlyAspAsnSerArgValValProLeuAspGluIleLysGluAlaAlaAlaAla 687
Db 3821 TATGGAGACAAACAGCCGGGTGTGTCTACAGGAAGAGATCGTGGGCGCAGCAAGGAGGCC 3880
Qy 688 AsnIleHisSerPheIleGluGlyLeuProGluLysTyrrAsnThrGlnValGlyLeuLys 707
Db 3881 ACATACATGCTTTCATTCGAGTCACTGCTCTAATAATATAGCACTAAAGTAGGAGACAA 3940
Qy 708 GlyAlaGlnLeuSerGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGln 727
Db 3941 GGAACTCAGCTCTCTGTGCCCAAGAAACAAACGATTCGCCATAGCTCTGCTGCTTTGTTAGA 4000
Qy 728 LysProLysIleLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLys 747
Db 4001 CAGCCTCATATTTTGTCTTGGATGAAGCCAGCTCAGCTCTGATACAGAAAGTGAAG 4060
Qy 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHis 767
Db 4061 GTTGTCCAGAGAGCCCTGGACAAAGCCAGAGAGGCGCCACCTGCTATTGTGATTGCTCAC 4120
Qy 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 4121 CGCTGTCCACCATCCAGAAATGAGACTTAATAGTGGTGTTCAGAAATGCGCAGAGTCAAG 4180
Qy 788 GluGlnGlyThrHisGlnLeuLeuLeuArgAsnArgAspIleTyrrPheLysLeuValAsn 807
Db 4181 GAGCATGGCAGCATCAGCAGCTGCTGGCAGAGAGGCGCATCTATTATTTTCAATGGTCACT 4240
Qy 808 AlaGlnSer 810
Db 4241 GTCCAGGCT 4249
RESULT 10
5206352-3
; Patent No. 5206352
; APPLICANT: Roninson, Igor B.; Paestan Ira H.; Gottesman,

QY	229	ProGluValSerLeuLeuLysIleLeuLysLeuAsnLysProGluThrProPheValVal	248
DB	2501	CTCCAGATTCCTTTGGAGGATTATGAAGCTAAATTTAACTGAATGGCCTTATTTTGT	2560
QY	249	LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIlePhe	268
DB	2561	GTGGGTATTTTGGCCATTATAAATGGAGCCCTGCACACAGCATTTGCCAATAATTT	2620
QY	269	AlaLysIleIleThrMetPheGlyAsn---AsnAspLysThrThrLeuLysHisAspAla	287
DB	2621	TCAAGATTATATAGGGTTTTTACAAGATTGTATGATCTCTGAACACAAACGACAGAACTACT	2680
QY	288	GluLeuTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMet	307

[illegible]

2861	GCATTGACTACCAAGCTGCCCAATGATGCTGCTCAAGTTTAAGGGGGCTATAGATTTCCAGG	2920
368	IIGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle	387
2921	CTTGCTGTAAATACCCAGAAATAGCAAACTCTGGCAGGAAATAATTATATCTCTTCATC	2980
388	TyrGlyTyrGluMetThrPheIleuIleLeuSerIleAlaProValLeuAlaValThrGly	407
2981	TATGGTTGGCAATACACGTTACTCTTAGCAATGTACCCCATCTTCGCAATGACAGA	3040
408	MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHis	427
3041	GTTGTTGAAATGAAATGTGTGCGACAAGCACTGAAAGATAAGAAAGAACTAGAAAGT	3100
428	AlaGlyLysIleAlaThrGlnAlaLeuGluAsnIleArgThrIleValSerLeuThrArg	447
3101	GCTGGGAAGATGCTACTGAAGCAATAGAAAACTTCCGAACCGTGTGTTCTTTTGACTCAG	3160
448	GluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSer	467
3161	GAGCAGAGTTTGAACATATGTTGCTCAGAGTTTGCAGGTACCATACAGAAACTCTTTG	3220
468	LysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAla	487
3221	AGGAAGACACACATCTTTGGAAATTACATTTTCCTTACCAGGCAATGATGATTATTTCC	3280
488	TyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGlu	507
3281	TATGCTGAGATTTTCGGTTTGAGCCCTACTTGTGGCACATAAACTCATGAGCTTTGAG	3340
508	GlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeu	527
3341	GATGTTCTGTAGTATTTTCAGCTGTGTCTTGTGGTGCATGCGCGTGGGGCAAGTCAGT	3400
528	ValLeuAlaProGluTyrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeu	547
3401	TCATTTGCTCTCTGACTATGCCAAGCAAAATATCAGCAGGCCACCATCATCATGATCAT	3460
548	GluLysLysProAsnIleAspSerArgGerGlnGluGlyLysLysProAspThrCysGlu	567
3461	GAATAAACCCCTTTGATTGACAGCTACAGCAGCGAAGCGCTAATGCCGAACACATTGGAA	3520
568	GlyAsnLeuGluPheArgGluValSerPhePheTyrProCysArgProAspValPheIle	587
3521	GGAATATGTCACATTTTGGTGAAGTTGTATTAACATATCCCAACCCGACCCGACATCCAGTG	3580

RESULT 11
US-08-793-610-5
Sequence 5, Application US/08793610
Patent No. 5858744
GENERAL INFORMATION:
APPLICANT: BAUM, Christopher
APPLICANT: STOCKING-HARBERS, Carol
APPLICANT: OSTERTAG, Wolfram
TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
TITLE OF INVENTION: FOR GENE TRANSFER
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKATADO, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793.610


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; LENGTH: 8630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: proviral
; OTHER INFORMATION: plasmid DNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(160)
; OTHER INFORMATION: plasmid backbone (pUC)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (161)..(677)
; OTHER INFORMATION: 5'-LTR
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (532)..(1219)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1220)..(5062)
; OTHER INFORMATION: m4 mdr-1 cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5215)..(5774)
; OTHER INFORMATION: 3'-LTR
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5775)..(8630)
; OTHER INFORMATION: plasmid backbone (pUC)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(8630)
; OTHER INFORMATION: retroviral expression vector SFbeta71m4
US-09-306-417-1

Alignment Scores:
Pred. No.: 2,23e-277 Length: 8630
Score: 2436.00 Matches: 466
Percent Similarity: 76.79% Conservative: 166
Best Local Similarity: 56.62% Mismatches: 177
Query Match: 59.72% Indels: 14
D5: 4 Gaps: 4

US-09-873-409-2 (1-812) x US-09-306-417-1 (1-8630)
Qy 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
Db 2576 GTTGATGACAGGATATTAGGACCATTAATGTAAGGTTTCTACGGAAATCATTTGGTGTG 2635
Qy 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
Db 2636 GTGAGTCAGGAACCTGTATTGTTGCCACCACGATAGCTGAAACATTCGCTATGGCCGT 2695
Qy 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyrAspPhe 61
Db 2696 GAAATGTCACCATGATGAGATTGAGAAAGCTGTCAAGGAAGCCATGCTATGACTTT 2755
Qy 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyAlaGlnMetSer 81
Db 2756 ATCATGAACATGCCTCATAAATTTGACACCCCTGTTGGAGAGAGAGGGCCGCTTGGAT 2815
Qy 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
Db 2816 GGTGGCAGAGAGCAGAGATGCCATTGCAGTCCCTGTTTCCCAACCCCAAGATCCTC 2875
Qy 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAlaAla 121
Db 2876 CTGTGGATGAGGCCACGCTGACCTTGACACCTGACACAGAAAGCGAAGCGTGTTCAGGTGGCT 2935
Qy 122 LeuGlnLysAlaSerLysGlyArgThrThrIleValValAlaAlaHisArgLeuSerThrIle 141
Db 2936 CTGGATAAGGCAGAAAGGTCGACCCACCAATTGTGTAGTTCATTCGTTTGTCTACAGTT 2995
142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyAlaHis 161
2996 CGTAATGCTGACATCGCTGCTGTTTCGATGATGGAGTCAATGTCGAGAAAGAAATCAT 3055
162 AlaGluLeuMetAlaLysArgGlyLeuTyrTyrSerLeuValMetSerGln----- 178
3056 GATGAACCTCATGAACAGAAAGCGCATTTACTTCANACTTGTCAACATGTCAGACAGCAGGA 3115
179 -----AspIleLysIleAlaAspGluGlnMetGluSerMetThrTyrSerThrGlu 195
3116 AATGAAGTTGAATTAGAAATGACGCTGATGATCCAAAGTCCAAAGTGAATGATGCTTGGAA 3175
196 ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209
3176 ATGCTCTCAATGATTCAAGATCCAGCTCTAATAAGAAAGAAAGATCAACTCGTAGGAGTGC 3235
210 Lys---SerAspPheIleAspLysAlaGluGluSerThrGlnSerLysGluIleSerLeu 228
3236 CGTGATCACAAGCCCAAGACAGAAAGCTTAGTACCAAGAGGCTCTGATGAAGATATA 3295
229 ProGluValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTrpProPheValVal 248
3296 CTCCAGTTTCCCTTTGGAGGATTGAAGCTAATAATTAACTGAATGGCCCTTATTTGTT 3355
249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
3356 GTTGGTGTATTGTCCTATTATAATGAGGCTGCAACAGCATTTGCAATAATATTT 3415
269 AlaLysIleIleThrMetPheGlyAsn---AsnAspLysThrThrLeuLysHisAspAla 287
3416 TCAAGATTTATAGGGTTTTTACAGAAATGATGATCCTGAAACAAACAGACAGATAGT 3475
288 GluIleTyrSerMetIlePheValIleLeuGlyValIleCysPheValSerTyrPheMet 307
3476 AACTGTTTTCATTTGTTTCTAGCCCTTGAAATTTATTTCTTTTATTACATTTTTCCTT 3535
308 GlnGlyLeuPheTyrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAla 327
3536 CAAGGTTTTCACATTTGGCAAGCTGGAGAGATCCTCACCAGCGCTCGATACATGGTT 3595
328 PheLysAlaMetLeuTyrGlnAspIleAlaTyrPheAspGluLysGluAsnSerThrGly 347
3596 TTCGATCCATGCTCAGACAGGATGTGAGTTGTTGATGACCTTAAACACCACCTGGA 3655
348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
3656 GCATTGACTACCAGGCTCCCAATGATGCTGCTCAAGTTAAAGGGCTATAGTTCCAGG 3715
368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
3716 CTGCTGTAAATTACCCAGATATAGCAATCTTGGACAGGAAATATATATATCTTCATC 3775
388 TyrGlyTrpGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGly 407
3776 TATGGTTGGCACTAACACACTGTTACTTCTTAGCAATTTGTACCCATCATTCGAATAGCAGGA 3835
408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHis 427
3836 GTTGTGAAATGAATGTTGTCTGCAAGCACTGCTGCAAGCACTGCTGCAAGCACTGAGGT 3895
428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArg 447
3896 GCTGGGAGATCGCTACTCAGCAATAGAAAACCTCCGAACCGTGTCTTCTTGACTCAG 3955
448 GluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
3956 GAGCAAGATTTGAACATATGATGCTCAGAGTTTGCAGGTTCACAGTACCAAGAACTCTTTC 4015
468 LysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleTyrPheAla 487
4016 AGGAAGACACACATCTTTGGAATTCATTTCTTCCACCCAGCATGATGATTTTTC 4075
488 TyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGlu 507

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Db 4076 TATGCTGGAGTTTCGGTTGGAGCTACTTGGTGGCACAATAAATCATGAGCTTTGAG 4135
Qy 508 GlyMetPheLeuValPheThrAlaLeuAlaLeuValPheThrLeu 527
Db 4136 GATGTTCTGTAGTATTTTCAGCTGTGCTTTGGTGGCCATGCGCTGGGCAAGTCAGT 4195
Qy 528 ValLeuAlaProGluThrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeu 547
Db 4196 TCATTGCTGCTGATCATCCAAAGCAAAATATCATCAGCGCCACATCATCATCAT 4255
Qy 548 GluLysLysProAsnLeuAspSerArgSerGlnGluLysLysProAspThrCysGlu 567
Db 4256 GAAATAACCCCTTTGATTGACAGCTACAGCAGGAGGCTAATGCGGACACATTTGGA 4315
Qy 568 GlyAsnLeuGluPheArgGluValSerPhePheTyProCysArgProAspValPheLe 587
Db 4316 GGAATATGTCACTTTGTAAGTTGTAATCAACTATCCACCGCCGACATCCCAAGT 4375
Qy 588 LeuArgGlyLeuSerLeuSerLeuGluArgGlyThrValAlaPheValGlySerSer 607
Db 4376 CTTGAGGAGTACCTGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4435
Qy 608 GlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyArgProValGlnGly 627
Db 4436 GCGTGTGGGAGAGCAGAGTGGTCCAGCTCTCGAGCGGTCTTACGACCCCTTGGCAG 4495
Qy 628 GlnValLeuPheAspGlyValAspAlaLysGluLeuAsnValClnThrPheArgSerGln 647
Db 4496 AAGTGTCTGTTGATGCGCAAGAAATTAAGCGACTGAATGTCAGTGGCTCCGAGCAC 4555
Qy 648 IleAlaLeuValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAla 667
Db 4556 CTGGGATCTGTCTCCAGGAGGCCATCTCTTTGACTGCGAGCATTCCTGAGAACATTC 4615
Qy 668 TyrGlyAspAsnSerArgValValProLeuAspGluLeuLysGluAlaAlaLeuAla 687
Db 4616 TATGGAGACAAACCGCGGTGTGTACAGAGAGATCTGAGGCGAGCAAGAGGAGGC 4675
Qy 688 AsnIleHisSerPheLeuGluGlyLeuProGluLysTyArgSerGlnValGlyLeuLys 707
Db 4676 AACATATGCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4735
Qy 708 GlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAlaLeuAlaArgAlaLeuGln 727
Db 4736 GGAATCTGCTCTGCTGCGCCAGAAACAGCATTCGCTGCTGCTGCTGCTGCTGCTG 4795
Qy 728 LysProLysIleLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLys 747
Db 4796 CAGCCTCATATTTGCTTTGGATGAGCGCCATGCTGCTGCTGCTGCTGCTGCTGCTG 4855
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Qy 788 GluGlnGlyThrHisGlnGluLeuArgAsnArgAspIleTyPheLysLeuValAsn 807
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Qy 808 AlaGlnSer 810
Db 5036 GTCCAGGCT 5044

RESULT 13
US-09-306-417-2
; Sequence 2, Application US/09306417
; Patent No. 6548301
; GENERAL INFORMATION:
; APPLICANT: Heinrich-Pette-Institut

; TITLE OF INVENTION: Retroviral Gene Transfer Vectors
; FILE REFERENCE: P50491
; CURRENT APPLICATION NUMBER: US/09/306.417
; CURRENT FILING DATE: 1999-05-06
; EARLIER APPLICATION NUMBER: DE 198 22 115
; EARLIER FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 8630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: proviral
; OTHER INFORMATION: plasmid DNA
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (1)..(8630)
; OTHER INFORMATION: retroviral expression vector SFbeta91mSA1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(160)
; OTHER INFORMATION: plasmid backbone (pUC)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (161)..(677)
; OTHER INFORMATION: 5'-LTR
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (532)..(1219)
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (1220)..(5062)
; OTHER INFORMATION: msal mdr1 cDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5215)..(5774)
; OTHER INFORMATION: 3'-LTR
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5775)..(8630)
; OTHER INFORMATION: plasmid backbone (pUC)
; OTHER INFORMATION: plasmid backbone (pUC)
US-09-306-417-2

Alignment Scores:
Pred. No.: 2,236-277 Length: 8630
Score: 2436.00 Matches: 466
Percent Similarity: 76.79% Conservative: 166
Best Local Similarity: 56.62% Mismatches: 177
Query Match: 59.72% Indels: 14
DB: 4 Gaps: 4

US-09-873-409-2 (1-812) x US-09-306-417-2 (1-8630)

Qy 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyArgAspHisIleGlyVal 21
Db 2576 GTTGTAGCAGAGATATTAGGACCAATAAATTAAGAGTTTCTACGGGAATCATTCGCTG 2635
Qy 22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyArg 41
Db 2636 GTGACTCAGGACCTGATTTGTTCCACAGCATAGTGAAACATTCGCTATGCGCT 2695
Qy 42 AspAspValThrAspGluGluMetGluArgAlaAlaArgGluAlaAsnAlaTyArgPhe 61
Db 2696 GAAATGTCCCATGTGAGATTGAGAAAGCTGTCAAGGAAGCAATGCCTATGACTTT 2755
Qy 62 IleMetGluPheProAsnLysPheAsnThrLeuValGlyGluLysGlyValaGlnMetSer 81
Db 2756 ATCATGAACCTGCTCATATAATTTGACACCTGTTGGAGAGAGAGGCGCCAGTTGAGT 2815
Qy 82 GlyGlyGlnLysGlnArgIleAlaIleAlaArgAlaLeuValArgAsnProLysIleLeu 101
Db 2816 GGTGGCAGAGCAGAGATGCGCATTCACGTGCCCTGTTGTCGCAACCAAGATCCTC 2875

QY 102 IleLeuAspGluAlaThrSerAlaLeuAspSerGluSerLysSerAlaValGlnAla 121
Db 2876 CTGCTGGATGAGGCAACGCTGACGCTTTGGACAGAAAGCGAGCGTGTTCAGTGGCT 2935
QY 122 LeuGluLysAlaSerLysGlyArgThrThrIleValAlaHisArgLeuSerThrIle 141
Db 2936 CTGTAAGGCGCAGAAAGGTCGACACCACTTGTGATAGTCATCGCTTGTCTACAGTT 2995
QY 142 ArgSerAlaAspLeuIleValThrLeuLysAspGlyMetLeuAlaGluLysGlyValAlaHis 161
Db 2996 CGTAATGCTGACGTCATCGCTGGTTTCGATGATGAGTCAATTTGGAGAAAGGAATCAT 3055
QY 162 AlaGluLeuMetAlaLysArgGlyLeuThrThrSerLeuValMetSerGln----- 178
Db 3056 GATCAACTCATGAAAGAGAAAGGCAATTACTTCAAACTTGTCAATGCACAGCAGCAGGA 3115
QY 179 -----AspIleLysLysAlaAspGluGlnMetGluSerMetThrThrSerThrGlu 195
Db 3116 AATGAAGTTGAATAGAAATGACGATGATCAATCCAAAGTGAATATGATGCTTGGAA 3175
QY 196 ArgLysThrAsnSerLeuProLeuHisSerVal-----LysSerIle 209
Db 3176 ATGCTTCAATGATCAAGATCCAGTCTAATAAGAAAGATCAACTCGTAGGAGTGTG 3235
QY 210 Lys---SerAspPheIleAspLysAlaGluGluSerThrGlnSerLysGluIleSerLeu 228
Db 3236 CGTGATCACAAAGCCCAAGCAGCAAGCTTAGTACCAAGAGCGCTCTGGATGAAGTATA 3295
QY 229 ProGluValSerLeuLeuLysIleLeuLysLeuAsnLysProGluTyrProPheValVal 248
Db 3296 CTCCAGTTTCTTTGGAGATATAGAGCTAATTTACTGAATGGCTTATTTTGT 3355
QY 249 LeuGlyThrLeuAlaSerValLeuAsnGlyThrValHisProValPheSerIleIlePhe 268
Db 3356 GTTGCTGTATTTTGTGCCATTAATAATGGAGCGCTGCAACACGAGCATTTGCAATAATTT 3415
QY 269 AlaLysIleIleThrMetPheGlyAsn---AsnAspLysThrThrLeuLysHisAspAla 287
Db 3416 TCMAAGATTATAGGGTTTTCAGGAATGATGATCTCTGMAACCAAAACGACAGAAATAGT 3475
QY 288 GluIleThrSerMetIlePheValIleLeuGlyValIleCysPheValSerThrPheMet 307
Db 3476 AACTTGTCTTCTATGCTTCTAGCCCTTGGATTTATTTCTTTATATATTTTCTT 3535
QY 308 GlnGlyLeuPheThrGlyArgAlaGlyGluIleLeuThrMetArgLeuArgHisLeuAla 327
Db 3536 CAAGTTTTCATTTGGCAAGCTGGAGAGATCTCCAAAGCGCTCCGATATCGTT 3595
QY 328 PheLysAlaMetLeuThrGlnAspIleAlaIlePheAspGluLysGluAsnSerThrGly 347
Db 3596 TTCGATCCATGCTCAGACAGGATGTGATGGTTTGTATGACCCCTAAACACCACTGGA 3655
QY 348 GlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaThrGlySerArg 367
Db 3656 GCATTGACTACCGCTCGCAATGATCTCTCAAGTTAAAGGGCTATAGGTTCAGG 3715
QY 368 IleGlyValLeuThrGlnAsnAlaThrAsnMetGlyLeuSerValIleIleSerPheIle 387
Db 3716 CTGCTGTAAATACCAAGATATAGCAAACTTGGGACAGGAATAATATATCTTCATC 3775
QY 388 TyrGlyTyrGluMetThrPheLeuIleLeuSerIleAlaProValLeuAlaValThrGly 407
Db 3776 TATGTTTGGCAACTAACACTGTACTCTTACCAATTTGATCCCATCATTTGCAATAGCAGGA 3835
QY 408 MetIleGluThrAlaAlaMetThrGlyPheAlaAsnLysAspLysGlnGluLeuLysHis 427
Db 3836 GTTGTGAAATGMAAATGTGTCTGGACAAGCAGCTGAAGATGAAGAAAGAACTAGAAGGT 3895
QY 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleLeuArgThrIleValSerLeuThrArg 447
Db 3896 GCTGGGAAGATGCTACTTACTGAAGCAATAGAAATCTCCGAAACCGTGTCTTCTTACTCAG 3955

QY 448 GluLysAlaPheGluGlnMetTyrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
Db 3956 GAGCAAGTTTGAACATATGATGCTCAGAGTTTGCAGGTACCATACAGAAACTCTTTC 4015
QY 468 LysLysAlaGlnIleIleGlySerCysTyrAlaPheSerHisAlaPheIleThrPheAla 487
Db 4016 AGGAAAGCAGCATCTTTCCGAATTACATTTCTTCCACCCAGGCAATGATTTTTC 4075
QY 488 TyrAlaAlaGlyPheArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGlu 507
Db 4076 TATGCTGGATGTTTCGGTTTGGAGCTACTTGGTGGCAGATAAACTCATGAGTTTGA 4135
QY 508 GlyMetPheIleValPheThrAlaIleAlaTyrGlyAlaMetAlaIleGlyLysThrLeu 527
Db 4136 GATGTTCTGTGTATTTTTCAGCTGTGTTCTTTGGTGGCAGTCCCTGGGCGAGTCAGT 4195
QY 528 ValLeuAlaProGluThrSerLysAlaLysSerGlyAlaAlaHisLeuPheAlaLeuLeu 547
Db 4196 TCATTTGCTTCTGACTATGCCAAGCCAAATATCAGAGGCCACATCATCATGATCAT 4255
QY 548 GluLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGlu 567
Db 4256 GAAAAACCCCTTGTATTGACAGCTACAGCAGGAGGCGCTAATGCCGAACACATTTGGA 4315
QY 568 GlyAsnLeuGluPheArgGluValSerPheThrProCysArgProAspValPheIle 587
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QY 588 LeuArgGlyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSer 607
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QY 608 GlyCysGlyLysSerThrSerValGlnLeuLeuGlnArgLeuTyrAspProValGlnGly 627
Db 4436 GGCCTGTGGAAAGACACAGCTGCTCAGCTCTCTGGAGCGGTTCTACACCCCTTGGCAGG 4495
QY 628 GlnValLeuPheAspGlyValAlaLysGluLeuAsnValGlnThrLeuArgSerGln 647
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QY 648 IleAlaIleValProGlnGluProValLeuPheAsnCysSerIleAlaGluAsnIleAla 667
Db 4556 CTGGGATCGTGTCCAGGAGGCCATCTCTGTTGATGTCAGCATTTGCTGAGAACATTTGC 4615
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Db 4616 TATGGAGACAACAGCCGGTGTGTACAGGAAGAGATCTGTGAGGCGCACAAGGAGGCC 4675
QY 688 AsnIleHisSerPheIleGluGlyLeuProGluLysThrAsnThrGlnValGlyLeuLys 707
Db 4676 AACATACATGCTTCATCGAGTCACCTGCTTAATAATATAGCACTAAAGTAGAGCAAA 4735
QY 708 GlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuLeuGln 727
Db 4736 GGAATCTAGCTCTCTGTTGGGCCAGAAACAACGATGCGCATAGCTCGTCCCTTGTAGA 4795
QY 728 LysProLysIleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLys 747
Db 4796 CAGCCTCATATTTTGTGATGAGCCAGCTCAGCTCTGATACAGAAAGTGAAGAAG 4855
QY 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValThrHis 767
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QY 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 4916 CGCTGTCTCCACCATCCAGAAATGCAGACTTAATAGTGTGTTTTCAGAAATGCGAGAGTCA 4975
QY 788 GluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleThrPheLysLeuValAsn 807
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QY 808 AlaGlnSer 810

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Db      5036 GTCCAGGCT 5044
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RESULT 14
US-08-793-610-6
; Sequence 6, Application US/08793610
; Patent No. 5858744
; GENERAL INFORMATION:
; APPLICANT: BAUM, Christopher
; APPLICANT: STOCKING-HARRIS, Carol
; APPLICANT: OSTERTAG, Wolfram
; TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
; TITLE OF INVENTION: FOR GENE TRANSFER
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,610
; FILING DATE: 07-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 31 973.8
; FILING DATE: 08-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 03 952.1
; FILING DATE: 07-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03175
; FILING DATE: 10-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Beiman, Richard J.
; REGISTRATION NUMBER: 39,105
; REFERENCE/DOCKET NUMBER: P1614-7007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9318 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
US-08-793-610-6

Alignment Scores:
Pred. No.:      2,55e-277      Length:      9318
Score:          2436.00      Matches:      466
Percent Similarity: 76.79%      Conservative: 165
Best Local Similarity: 56.62%      Mismatches:  177
Query Match:     59.72%      Indels:       14
DB:              2          Gaps:         4

US-09-873-409-2 (1-812) x US-08-793-610-6 (1-9318)
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Db      3132 GTTGATGGACAGGATATAGGACCATTAATGTAAAGTTTCTACGGGAATCATTTGGTGG 3191
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Qy      22 ValSerGlnGluProValLeuPheGlyThrThrIleSerAsnAsnIleLysTyrGlyArg 41
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Db      3192 GTGAGTCAGGAACCTGTATTGTTGGCCACCAGCATAGCTGAAACACATTTCGTATGCCGT 3251
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Qy      42 AspAspValThrAspGluGluMetGluArgAlaLeuArgGluAlaAsnAlaTyrAspPhe 61
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Db 4332 TATGCTTGGCACTAAACACACTGTTACTCTTACCAATTTGATCCCATCTTGCATATAGCAGGA 4391
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Db 4392 GTTGTGTAATGAAATGTTGTTCTGGCAACGACTGAAGATAGAAAGAACTAGGAAGGT 4451
Qy 428 AlaGlyLysIleAlaThrGluAlaLeuGluAsnIleArgThrIleValSerLeuThrArg 447
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Qy 448 GlnLysAlaPheGluGlnMetThrGluGluMetLeuGlnThrGlnHisArgAsnThrSer 467
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Qy 488 TyrAlaAlaGlyPheArgPheGlyValTyrLeuIleGlnAlaGlyArgMetThrProGlu 507
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Qy 548 GlnLysLysProAsnIleAspSerArgSerGlnGluGlyLysLysProAspThrCysGlu 567
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Qy 568 GlyAsnLeuGluPheArgGluValSerPhePheTyrProCysArgProAspValPheIle 587
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Qy 608 GlyCysGlyLysSerThrSerValGlnLeuGlnArgLeuTyrAspProValGlnGly 627
Db 4992 GGCTGTGGAGAGACACACAGTGTCTGAGTGTCTGAGCGGTCTACGACCCCTTGGCAGGG 5051
Qy 628 GlnValLeuPheAspGlyValAspAlaLysGlnLeuAsnValGlnThrLeuArgSerGln 647
Db 5052 AAGTGTGCTGTGATGCAAGAAATAAAGCGACTGAATGTTTCACTGCTGCTGCTGCTGCTG 5111
Qy 648 IleAlaIleValProGlnGluProValIleuPheAsnCysSerIleAlaGluAsnIleAla 667
Db 5112 CTGGGATCGTGTCCAGGAGCCCATCTGTTTACTGTCAGCATGCTGTCAGACATGCTCC 5171
Qy 668 TyrGlyAspAsnSerArgValProLeuAspGluIleLysGluAlaAlaAsnAlaAla 687
Db 5172 TATGAGACACACACCGGTTGTGTACAGAGAGATCTGTAGGCGCAGCAAGAGAGGCC 5231
Qy 688 AsnIleHisSerPheIleGluGlyLeuProGluLysTyrAsnThrGlnValGlyLeuLys 707
Db 5232 AACATACATGCTTTCATCGAGTCTCTGCTTAAATAATATAGCATTAAGTAGGAGACAAA 5291
Qy 708 GlyAlaGlnLeuSerGlyGlyGlnLysGlnArgLeuAlaIleAlaArgAlaLeuGln 727
Db 5292 GGAATCAGCTCTCTGTTGGCCAGAAACAGCATTCGCATAGCTCTGCTGCTGCTGCTGCTG 5351
Qy 728 LysProLysIleLeuLeuLeuAspGluAlaThrSerAlaLeuAspAsnAspSerGluLys 747
Db 5352 CAGCTCATATTTTGTCTTTTGGATGAAGCCACGTCAGCTCTGGATACAGAAAGTGAAG 5411
Qy 748 ValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThrHis 767
Db 5412 GTTGTCCAGAGACCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5471

Qy 768 ArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIleLys 787
Db 5472 CCCTGTCCACCATCCAGATCCAGATCTTAATAGTGGTGTTCAGATGGCAGAGTCAAG 5531
Qy 788 GluGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeuValAsn 807
Db 5532 GAGCATGGCAGCATCAGCAGCTGTGGCAGAGAAAGGCATCTATTTTCAATGGTCACT 5591
Qy 808 AlaGlnSer 810
Db 5592 GTCCAGGCT 5600
RESULT 15
US-09-120-513-1
; Sequence 1, Application US/09120513
; Patent No. 6025150
; GENERAL INFORMATION:
; APPLICANT: Brun, Kimberly
; APPLICANT: Chenery, Richard
; APPLICANT: Eilens, Harma
; APPLICANT: Field, John
; APPLICANT: Yue, Lin
; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE
; TITLE OF INVENTION: SEQUENCES ENCODING RAT MDR1B2 AND
; TITLE OF INVENTION: SCREENING METHODS THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: US
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,513
; FILING DATE: 22-JUL-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GP50008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5015
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4233 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-120-513-1
Alignment Scores:
Pred. No.: 2,95e-275 Length: 4233
Score: 2413.50 Matches: 467
Percent Similarity: 76.03% Conservative: 158
Best Local Similarity: 56.81% Mismatches: 180
Query Match: 59.17% Indels: 17
DB: 3 Gaps: 5
US-09-873-409-2 (1-812) x US-09-120-513-1 (1-4233)
Qy 2 ValAspGluAsnAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyVal 21
Db 1376 ATCGACGGACAGCAGCATCAGGACCATCATGAGGTATCTCGGGAATCATCTGGGGTG 1435


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Db      3590 AGACAGCCTCACATCTTACTTCTGATGAAGCGACATCAGCTCTGGATACGGAGAGTGAA 3649
Qy      747 LysValValGlnHisAlaLeuAspLysAlaArgThrGlyArgThrCysLeuValValThr 766
Db      3650 AAGTCTCTCCAGGAAGCGCTGACAAAGCCAGGAGAGCGCCACCTGCATTGGATCGCG 3709
Qy      767 HisArgLeuSerAlaIleGlnAsnAlaAspLeuIleValValLeuHisAsnGlyLysIle 786
Db      3710 CACCGCTGTCCACCATCCAGAACCGCAGACTTGTATCTGTGATTTCAGAACGGCCAGGTC 3769
Qy      787 LysGlnGlnGlyThrHisGlnGluLeuLeuArgAsnArgAspIleTyrPheLysLeuVal 806
Db      3770 AAGGAGCACCGGCACCCACCGCAGCTGTGCGCCAGAAAGGCATCTATTTCGATGGTT 3829
Qy      807 AsnAla 808
Db      3830 CAGGCT 3835

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Search completed: June 25, 2004, 01:42:10
 Job time : 285 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 01:37:23 ; Search time 218 Seconds
(without alignments)
7270.366 Million cell updates/sec

Title: US-09-873-409-10

Perfect score: 2856

Sequence: 1 cctaatctctaatatctc.....atgcacagtcagtcagtgga 2856

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 27745446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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5: /cgm2_6/ptodata/2/ina/POCUS-COMB.seq.*

6: /cgm2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1030.2	36.1	3988	4	US-09-762-195-1
2	1030.2	36.1	4646	1	Sequence 1, Appli
3	1030.2	36.1	4646	1	Sequence 2, Appli
4	1030.2	36.1	4669	6	Sequence 1167, Ap
5	1030.2	36.1	6505	2	Patent No. 5206352
6	1030.2	36.1	9318	2	Sequence 5, Appli
7	1028.6	36.0	4264	2	Sequence 6, Appli
8	1028.6	36.0	4264	2	Sequence 1, Appli
9	1028.6	36.0	8630	4	Sequence 5, Appli
10	1027.2	36.0	3924	4	Sequence 2, Appli
11	1027.2	36.0	3924	4	Sequence 1168, Ap
12	1027.2	36.0	8630	4	Sequence 2, Appli
13	1025.4	35.9	4669	2	Sequence 1, Appli
14	1022.2	35.8	4669	2	Sequence 18, Appli
15	1022.2	35.8	4669	4	Sequence 1, Appli
16	1022.2	35.8	4669	4	Sequence 1, Appli
17	1020.6	35.7	4186	4	Sequence 1, Appli
18	1020.6	35.7	4186	4	Sequence 3, Appli
19	953.2	33.4	4233	3	Sequence 1, Appli
20	953.2	33.4	4233	3	Sequence 1, Appli
21	856	30.0	2726	1	Sequence 1, Appli
22	478	14.7	4175	4	Sequence 1, Appli
23	414.6	14.5	4002	2	Sequence 3, Appli
24	414.6	14.5	4002	2	Sequence 1, Appli
25	414.6	14.5	4002	2	Sequence 3, Appli
26	414.6	14.5	4002	3	Sequence 1, Appli
27	383.8	13.4	2698	4	Sequence 2, Appli

28	374	13.1	4047	2	US-08-612-734B-1	Sequence 1, Appli
29	329.6	11.5	3512	4	US-09-749-340-7	Sequence 7, Appli
30	309.2	10.8	4224	1	US-08-612-521-1	Sequence 1, Appli
31	302	10.6	4800	2	US-08-612-734B-3	Sequence 3, Appli
32	297	10.4	2681	4	US-09-749-340-8	Sequence 8, Appli
33	283.2	9.9	3924	1	US-08-395-246C-1	Sequence 1, Appli
34	225.8	7.9	1123	4	US-09-614-912-159	Sequence 159, Appl
35	224	7.8	224	4	US-09-614-912-159	Sequence 94, Appl
36	207.2	7.3	1185	4	US-09-614-912-161	Sequence 161, App
37	202.2	7.1	1053	4	US-08-956-171E-796	Sequence 796, App
38	198.4	6.9	1749	4	US-09-134-001C-1893	Sequence 1893, Ap
39	197.4	6.9	3792	4	US-09-351-224B-10	Sequence 10, Appl
40	197.4	6.9	3792	4	US-09-677-488A-10	Sequence 10, Appl
41	197.4	6.9	3792	4	US-09-677-682B-10	Sequence 1, Appli
42	196	6.9	3927	2	US-08-996-644-1	Sequence 1, Appli
43	196	6.9	3927	3	US-09-352-552-1	Sequence 3, Appli
44	195.2	6.8	3924	2	US-08-996-644-3	Sequence 3, Appli
45	195.2	6.8	3924	3	US-09-352-552-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-762-195-1
; Sequence 1, Application US/09762195
; Patent No. 6677319
; GENERAL INFORMATION:
; APPLICANT: Stremmel, Wolfgang
; TITLE OF INVENTION: Phosphatidylcholine as Medication with
; TITLE OF INVENTION: Protective Effect on Large Intestinal Mucosa
; FILE REFERENCE: 34691/208520
; CURRENT APPLICATION NUMBER: US/09/762,195
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: PCT/EP99/02426
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 198 35 526 2 DE
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 198 57 570.8 DE
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3988
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-762-195-1

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Best Local Similarity	62.2%;	Pred. No.	2.3e-288;						
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QY	166	ATTATTTGATAGAAACCCAGTATAGATTAACCTTTTCCACAGCTGGATATAAAAGCTGAATCC	225						
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QY	226	ATAGAAGCAACTGTGGAAATTTAAAAATGTTCTTTTCAATATTCCATTCAGAGCCATCTATC	285						
DB	1228	ATTAAGGGAATTTGGAAATTCGAAATGTTCACTTCAGTTACCCATCTCGAAAGAAGTT	1287						
QY	286	AAGATTTCTGAAAGGCTCTGAATCTCAGAAATTAAGTCTGGAGAGACAGCTGCGCTTGGTCGGT	345						
DB	1288	AAGATCTTTGAAGGGTCTGAAACCTGAAGGTGCAAGTGGGACAGACGGTGGCCCTTGGTTGGA	1347						
QY	346	CTCAATGGCAGTGGGAAAGAGTACGGTAGTCCAGCTTCTTCGACAGAGGTTATATGATCCGGAT	405						
DB	1348	AACAGTGGCTGTGGGAGAGACAAACAGTCCAGCTGATGACAGAGGCTCTATGACCCACA	1407						
QY	406	GATGCTTTTATCATGCTGGATGAGAAATGACATCAGAGCTTTTAAATGTGGGCAATATGCA	465						
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QY	466	GACCATAATGGAGTGGTATTAGTCAAGAGCCTGTTTTGTCGGGACCCACCATCATGATACAAAT	525						

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Db	1588	AATGCCATTGACTTTTATCATGAAACTGCTCATAAATTTGACACCCCTGGTTGGAGAGAGA	1647
Qy	646	GGAGCTCAAAATGAGTGGAGGSCAGAAACAGAGAGTCCCAATGCTGCTGCTTAGTTTGA	705
Db	1648	GGGCCCCAGTTGAGTGGGACAGAGCAGAGGATCGCCATTGCACGTGCCCTGGTTTCGC	1707
Qy	706	AAACCCCAAGATTTCTGATTTTATAGATGAGGCTACGTTCTCCCTGGATTCAGAAACGAATCA	765
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Qy	766	CTCTGTTCAAGCTGCACTGGAGAGCGCGAGAAAGGTCGAGACTCAATCTGCTGATGACAC	825
Db	1768	GTGGTTACAGTGGGCTCTGGATTAAGGCCAGAAAGAGTCGAGACCACTTTGTGATAGCTCAT	1827
Qy	826	CGACTTTTCTACTATTCCGAAGTGCAGATTTGATTTGTGACCCCTAAAGGATGGAATCTCGCG	885
Db	1828	GGTTTGTTCTACAGTTCGTTAATGCTGACGTCATCGCTGTTTCGATGATGAGTCAATTTGTG	1887
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Db	1888	GAGAAAGGAAATCATGATGAATCACTCATGAAGAGAAAGGCAATTTACTTTCAAATCTGTACA	1947
Qy	946	TCACAGGATATTAAANAAGCTGATGAACAGATGGAGTCAATGACATATTCTA	997
Db	1948	ATGCAGACAGCAGGAAATGAAGTTGAATAGAAATGCGAGTGAATCCAAAGTGAA	2007
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Db	2008	ATTGATGCCTTTGGAAATGCTCTTCAAATGATTTCAAGATCCAGTCTAATAAGAAAAAGATCA	2067
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Db	2488	AAAAACACCACTGGAGCATTTGACTACAGGCTCCCAATGATGCTGCTCAAGTTAAAGGG	2547
Qy	1504	GCAACAGGTTCCAGGATTTGGCGTCTTAAACAAAAATGCAACTAATCAGGACTTTTCAAGTT	1563

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1564	QY	ATCATTTCCCTTTATATATAGATGGAGATGACATTTCTCGATTTCTGAATATTCGATATATGCTCCAGTA	1623
2608	DB	AATATATCCCTTCATCTATGGTTGGACATAACACTGTTACTCTTTAGCAATGTTACCCATC	2667
1624	QY	CTTGCCCTGACAGGAATGATTTGAAACCGCAGCAATGACTGCGATTTGCCAACAAGATAAG	1683
2668	DB	ATTGCAATAGCGGAGTTGTTGAAATGAAATGTTGTCTGGAACAAGCACTGAAAGATAAG	2727
1684	QY	CAAGAACTTTAAGCATGCTGCAAGATAGCAACTGAAAGCTTTGGAGAATATACGTACTATA	1743
2728	DB	AAAGAACTAGAGGTGCTGGAGATCGCTACTGAGCAATAGAAACTTCCGAAACGGTT	2787
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2968	DB	CTCATGAGCTTTTGAGGATGTTCTGTTAGTATTTTTCAGCTGTGCTTTGGTGCATGCCC	3027
1984	QY	ATCGGAAAAACGCTTCGTTTTGGCTTCCTGAAATATTCCAAAGCCAAATCGGGGCTGGCCAT	2043
3028	DB	GTGGGCAAGTCAGTTCAATTTGCTCTGACTATGCCAAAGCCAAATATCAGCAGCCAC	3087
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3088	DB	ATCATCATGATCATTTGAAAAACCCCTTTCATTTGACAGCTACAGCAGGAAGCCCTAATG	3147
2104	QY	CCAGACACATGTGAAGGGAATTTAGAGTTTCGAGAAGTCTCTTTCTTCTATCCATGTGCG	2163
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2464	QY	GCCGCAATGCAAGCAATATCCATCTTTTATTTGAGGTTCTCCCTGAGAAATACACACA	2523
3508	DB	GCAGCAAGGAGGCAACATACATGCTTTCATCGAGTCACTGCTTATTAATATAGCACT	3567
2524	QY	CAAGTTCGACTGAAAGGAGCACAGCTTTCTGGGGCCAGAAAAAAGAGCTTAGCTATTGCA	2583
3568	DB	AAAGTAGAGNCAAGGAATCTAGCTCTCTGTGTGCCAGAAAA CAA CGCATTTGCCATGCT	3627
2584	QY	AGGCTCTTCTCCAAAAACCAAAATTTTATTTGTTGAATGAGGCCACTTCAGGCCCTCGAT	2643
3628	DB	CGTGCCTTGTTCACAGAGCTCTATTTTCTTTTGGATGAGCCAGTCAAGCTCTGGAT	3687

Db 2606 TTTGCAATAATATTTTCAAGATATATAGGGTTTTTACAGAAATGATGATCCCTGAACA 2665
 Qy 1267 AAG---CATGATGCAAGAAATTTATTCATGATATTTGTCATTTTGGGTGTTATTTGCTTT 1323
 Db 2666 AAAACACAGAAATAGTAATCTGTTTCTCACTATTTTCTAGCCCTTGAATATTTCTTTT 2725
 Qy 1324 GTACGATTTATTCATGCGAGGATTTATTTACGCGAGAGCAGGAGAAATTTTAAACATGAGA 1383
 Db 2726 ATTACATTTTCTTTCAGGGTTTACATTTGGCAAGCTGGAGAGATCTCTCACAGCGG 2785
 Qy 1384 TTAAGACACTTTGGCTTCAAGCCATGTTATATCAGGATATTTGCTGTTTGTATGAAAG 1443
 Db 2786 CTCGATACATGTTTTCGATTCATGCTCAGACAGGATGAGTGGTTGTTGATGACCT 2845
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 Qy 1504 GCAACAGGTTCCAGGATTTGGGTCTTTACACAAATGCAATTAACATGGGACTTTTCAGTT 1563
 Db 2906 GCTATAGGTTCCAGGCTTGTGTAATTAACAGAAATATAGCAATTTTGGACAGGAATA 2965
 Qy 1564 ATCATTTCTTTATATATGATGGATGGAGATGATCTCTGATTTCTGATATTTGCTCCAGTA 1623
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 Db 3026 ATTCAATAGCAGGATTTGTTGAAATGAAATGTTCTGCAAGCACTGAAGATAG 3085
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 Db 3086 AAAGAACTTAGAGGTGCTGGGAAGATGCTACTGAAGCAATAGAAATCTTCGAAACGTT 3145
 Qy 1744 GTGTCAATTAACAGGGAAGAAAGCCCTTCAGGCAATGATGAAGAGATGCTTCAGACTCAA 1803
 Db 3146 GTTCTTTGACTCAGGACAGAGATTTGAAATATATGATGCTCAGAGTTTGCAGTACCA 3205
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 Db 3206 TACAGAAATCTTTGAGGAAAGCACAATCTTTGGAATTAATTTCTTCCACCCAGGCA 3265
 Qy 1864 TTTATATATTTTCTGATGAGAGGTTTTCGATTTGGAGCTTATTTAATTCAGCTGGA 1923
 Db 3266 ATGATGATTTTCTATGCTGATGTTTCGTTTGGAGCTACTTGGTGGCACATAA 3325
 Qy 1924 GCAATGACCCAGAGGCAATGTTATGTTTACTGCAATTTGATGAGCTATGGCT 1983
 Db 3326 CTCATGAGCTTTGAGGATGTTCTGTTAGTATTTTTCAGCTGTTGTTTGGTGGCATGCC 3385
 Qy 1984 ATCGAATAACGCTGTTTGGCTCTGAAATATTCGAAGCCCAATCGGGGCTGCCAT 2043
 Db 3386 GTGGGCAAGTCAGTTTCTGCTGCTGATGCTCAAGCCCAATATACGACGCCAC 3445
 Qy 2044 CTGTTTGGCTTTTGGAAAGAAACCAATATAGACAGCCGCTCAAGAGGGGAAAG 2103
 Db 3446 ATCATCATGATCATTTGAAAGAAACCCCTTTGATTCAGAGCTACAGCACGGAAGGCTAATG 3505
 Qy 2104 CCAGACACATGTAAGGAAATTTAGATTTTCGAGAAGTCTTTCTTCTATCCATGCTGC 2163
 Db 3506 CCGAACACATTTGAGGAAATTTGCAATTTTGGTGAAGTTGTTTCAACTATCCACCCGA 3565
 Qy 2164 CCAGATGTTTTCATCTCCGCTGCTTATCTCCTCAGTATTTGAGGAGGAAAGACAGTAGCA 2223
 Db 3566 CCGGACATCCAGTCTTCAGGACTGAGCTGAGGCTGAGAGGCGCCAGACCTGCT 3625
 Qy 2224 TTTGTTGGGAGAGGCTGTTGGGAAAGCACTTCTGTTTCACTTTCTGACAGACTTTAT 2283
 Db 3626 CTGTGGGACAGGCTGTTGGGAAAGACAGTGTGCTCCAGCTCTTGGAGCGGTTCTAC 3685
 Qy 2284 GACCCGTTGCAAGGCAAGTGTGTTTCTGATGCTGTTGATGCAAGAAATTAAGATGTACAG 2343
 Db 3686 GACCCCTTGGCAGGGAAGTGTCTGTTGATGCTGCAAGAAATTAAGCCACTGAATGTTTACAG 3745

RESULT 3

US-09-023-655-1167
 : Sequence 1167, Application US/09023655
 : Patent No. 6607879
 : GENERAL INFORMATION:
 : APPLICANT: Cocks, Benjamin G.
 : APPLICANT: Susan G. Stuart
 : APPLICANT: Jeffrey J. Seilhamer
 : TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 : TITLE OF INVENTION: EXPRESSION
 : NUMBER OF SEQUENCES: 1508
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 : STREET: 3174 PORTER DRIVE
 : CITY: PALO ALTO
 : STATE: CALIFORNIA
 : COUNTRY: USA
 : ZIP: 94304
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/023,655
 : FILING DATE: HEREMITH
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER:
 : FILING DATE:
 : CLASSIFICATION:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Zeller, Karen J.
 : REGISTRATION NUMBER: 37,071
 : REFERENCE/DOCKET NUMBER: PA-0001 US

Qy 2344 TGCTCCGTTTCCAAATAGCAATCGTTTCTCAAGAGCCTGTGCTCTTCACTGAGCAATT 2403
 Db 3746 TGCTCCGAGCACAACCTCGGCGATCGTGTCCAGGAGCCCATCTGTTGATCGACGCAATT 3805
 Qy 2404 GCTGAGAAACATCGCTTATGTCACAAACAGCCGCTGTGTGTCATAGATGAGATCAAGAA 2463
 Db 3806 GCTGAGAAACATCGCTTATGTCACAAACAGCCGCTGTGTGTCACAGAGAGATCGTGAGG 3865
 Qy 2464 GCCGAAATGACAGCAATATTCATCTTTTATTTGAAGGTCTCCCTGAGAAATACACACA 2523
 Db 3866 GCAGCAAGAGGAGCCCAACATACATGCTTTCATCGAGTCTACTGCTTAATAATATAGCACT 3925
 Qy 2524 CAAATTTGGAAGTGAAGAGGACACAGCTTTCTGGCGGCAGAAACAAAGACTTAGCTATTGCA 2583
 Db 3926 AAGTAGAGGACAAAGAACTCAGCTCTCTGTGGCCAGAAACAGCAATGCTGCTAGCT 3985
 Qy 2584 AGGCTCTTCTCCAAACCCAAATTTTATTTGTTGATGAGGCCACTTCAGCCCTCGAT 2643
 Db 3986 CGTGCCCTTGTGTAGACAGGCTCATATTTTGTCTTTTGGATGAAGCCACGTCAGCTCGAT 4045
 Qy 2644 AATGACAGTGAAGAGGTGTTTCAAGCATGCCCTTGTATAAAGCCAGGACGGAGGACATGC 2703
 Db 4046 ACAGAAAGTGAAGAGGTGTTTCAAGAGCCCTGCAAGAGCCAGAGGCGCCACCTGC 4105
 Qy 2704 CTAGTGTCTCCTCAGAGGCTCTCTGCAATTCAGAACGCGAGATTTGATGTTGTTCTGCAC 2763
 Db 4106 ATTGTGATTTGCTCAGCCCTGTCCACCATCCAGATCCAGACTTAATAGTGTGTTTTCAG 4165
 Qy 2764 AATGGAAGTAAAGCAAGCAAGCACTCATCAAGCTCTCAGAGCTCTGAGAAATCGAGACATAT 2823
 Db 4166 AATGGCAGAGTCAAGGAGCATGCGCATCGAGCTGCTGCGCAGAAAGGCGCATCTAT 4225
 Qy 2824 TTTAAGTTAGTGAATGCACAGTCAG 2848
 Db 4226 TTTTCAATGTCAGTGTCCAGGCTG 4250

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1167
SEQUENCE CHARACTERISTICS:
LENGTH: 4546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g187468
US-09-023-655-1167

Query Match	36.1%	Score 1030.2	DB 4	Length 4646
Best Local Similarity	62.2%	Pred. No. 2.5e-288		
Matches 1695	Conservative 0	Mismatches 988	Indels 42	Gaps 3
Qy	166	ATTATTGATTAAGAAACCCAGATAGATAA	CTTTTCCACAGCTGGATATAAACCTGAATCC	225
Db	1526	ATATTGATTAATAGCCAAAGTATTGACAGCTATTGGAAGTGGGCACATCCAGATAA	T	1585
Qy	226	ATAGAAAGAACTGTGGAAATTTAAAAATGTTTCTTTCAATTATCCATCAAGACCATCTATC	285	
Db	1586	ATTAAAGGCAAAATTTGGAATTCAGAAATGTTTCACCTTCAGTTACCCATCTCGAAAGAAAGTT	1645	
Qy	286	AAGATTTCTGAAGAGTCTGAACTTCAGAAATTAAGTCTGGAGAGACAGTCGCTTGGTGGTGGT	345	
Db	1646	ARGATCTGAAGGGCCCTTGAACTTGAAGGTGACAGATGGGACAGCGTGGCCCTGGTTGGGA	1705	
Qy	346	CTCAATGGCAGTGGGAAGAGTACGGTAGTCCAGCTCTTCGACAGAGTTATATGATCCGGAT	405	
Db	1706	AACAGTGGCTGTGGGAAGAGCACAAACAGTCCAGCTGATGCAGAGGCTCTATGACCCACACA	1765	
Qy	406	GATGGCTTTATCATGGTGGATGAGAAATGACATCAGAGCTTTAAATGTGGGCATTATCGA	465	
Db	1766	GAGGGGATGGTCAGTGTGTGATGGAACAGGATATTAGGACCAATAAATGTAAAGTTTCTACGG	1825	
Qy	466	GACCATATTGGAGTGGTTAGTCAAGAGCGCTGTTTGTTCGGGACCCACCATCAGTAACAAT	525	
Db	1826	GAATCATTTGGTGGTTCAGTCAGGAACCTGTATTGTTTCCCAACCATAGCTGAATAC	1885	
Qy	526	ATCAAGTATGGAACAGATATGATGTGACTGTATGGAAGAGATGGAGAGACAGCAAGGAAGCA	585	
Db	1886	ATTGCTATTGGCCGTGAAATGTCAACATGGAATGAGATGGAAGAGTGTCAAGGAAGCC	1945	
Qy	586	AATCGCTATGATTTTATCATGGAGTTCCTAAATAAATTTAATACATTTGGTAGGGGAAATA	645	
Db	1946	ATNGCCTATGACTTTATCATGAAACTGCTCTATAAATTTGACACCTGTGTTGGAGAGA	2005	
Qy	646	GGAGCTCAAAATGAGTGGAGGCGCAAAAACAGAGGATCGCAATGCTCTGCTCTTAGTTTGA	705	
Db	2006	GGGSCCCAGTTGAGTGGTGGGCAAGACAGAGGATCGCCATTGCAGTCGCCCTGGTTCCG	2065	
Qy	706	AACCCCAAGTCTTGATTTTATGATGAGGCTACGCTTCGCCCTGGATTGAGAAAGCAAGTCA	765	
Db	2066	AACCCCAAGATCCCTCCCTGCTGGATGAGGCGCACGTCAGCCTTGGACACAGAAAGCGAAGCA	2125	
Qy	766	GCTGTTCAAGCTGCATCTGGAGAAAGCGGAGCAAAAGGTCGGAACCTCAATTCGTGGTAGCACAC	825	
Db	2126	GTGGTTTCAGGTGGCTCTGGATAAGGCCAGAAAGGTCGAGACCACTTGATGATAGCTCAT	2185	
Qy	826	CGACTTTCTACTATTGGAAGTGCAGATTTGATTTGTGACCTTAAGAGATGGAATGCTGGCG	885	
Db	2186	CGTTTGTCTACAGTTCGTAAATGCTGAGCTCAATGCTGCTTTCGATGATGAGTCAATTGTG	2245	
Qy	886	GAGAAAGGAGCACATGCTGAACTAATGGCAAAACGAGGCTCTATATTATTCACTTGTGATG	945	
Db	2246	GAGAAAGGAATCATGATGAACTCATGAAAGAGAAGGCAATTACTTCAAACTTGTGACACA	2305	
Qy	946	TCACAGGATATTAAAAAGCTGATGAACAGATGGAGTCAATATGATATTCTA	997	
Db	2306	ATGCAGACAGCAGGAAATGAAGTTGAATTAGAAAAATGCAGCTCATGATTAATCCAAAGATGAA	2365	

Qy	998	-----CTGAAGAAAGAACCACTCACTCTCTCTGCACTCTCTGTGGAGAGCATCA---	1045
Db	2366	ATTGATGCCCTTGGAAATGTCTTCAAAATGATTTCAAGATCCAGTCTAATATGAAAAGATCA	24255
Qy	1046	-----AGTCAGACTTCATTGACAAGGCTGAGGAATCCACCCAATCT	1086
Db	2426	ACTCGTAGGAGTGTCCGTGGATCACAAGCCAAAGACAGAAAGCTTAGTACCAAGAGGCT	2485
Qy	1087	AAAGAGATAGTCTTCTGAAAGTCTCTCTATTAATAATTTTAAAGTTAAACAAGCCTGAA	1146
Db	2486	CTGGAATGAAGATATACCTCCAGTCTTCTTTGGAGGATTAAGAAGCTTAAATTTAACTGAA	2545
Qy	1147	TGGCCCTTTGTGGTTCTGGGGCAATGGCTTCTGTTCTCTAAATGGAACTGTTCTATCCAGTA	1206
Db	2546	TGGCCCTATTTGTGTGTGGTATTTTGTGCCATTATAAATGGAGCCTGCAACAGCA	2605
Qy	1207	TTTTCCATCATCTTTGCAAAAATATATAACAATGTTGGAAATATATGATAAAACCAATTA	1266
Db	2606	TTTGCATAATAATTTTCAAAAGATTATAGGGGTTTTTACAGAAATGATGATCCTGAAACA	2665
Qy	1267	AAG---CATGATGCAGAAATTTATTCATGATATTCGTCTCAATTTTGGGTGTTATTTGCTTT	1323
Db	2666	AAACGACAGAAATAGTAACTTGTTTCACTATTTGTTCTAGCCCTTGGAAATATTTCTTTT	2725
Qy	1324	GTCAATTATTTTCATGAGGATTTATTTTACGCGAGAGCAGGGGAAATTTTAAAGATGAGA	1383
Db	2726	ATTACATTTTCTTTCAGGGTTTCACTTTGGCAAAGCTGGAGAGTCTCCACCAAGCGG	2785
Qy	1384	TTAAGACATTTGGCCTTCAAAGCCATGTTTATATCAGGATATTCCTGGTTTGATGAAAG	1443
Db	2786	CTCGATACATGTTTTCOGATCCATGCTCAGACAGGATGTGTAGTTGGTTTGATGACCTT	2845
Qy	1444	GAACACAGCACAGGAGGCTTGACAACAATAATTAGCCATAGATATAGCACAATTTCCAGGA	1503
Db	2846	AAAAACACCACTGGAGCATTTGATACAGGCTCGCCAATGATCTGCTCAAGTTAAAGGG	2905
Qy	1504	GCACAGGTTTCCAGGATTTGGCGTCTTAAACAACAAATGCAACTAACATGGGACTTTTCAATT	1563
Db	2906	GCTATAGTTTCCAGGCTTGCTGTAATTACCCAGAAATATAGCAAACTTTGGGACAGGAATA	2965
Qy	1564	ATCATTTCTTTATATATGATGGAGATGACATTTCTGATTTCTGAGTATTTGCTCCAGTA	1623
Db	2966	ATTATATCTTCACTATGTTTGGCAACTTAACACTGTTACTCTTAGCAATTTGATCCCATC	3025
Qy	1624	CTTGGCGTGCACGGAATGATTTGAACCGGACGCAATGACTGGATTTGCAACAAGATAAG	1683
Db	3026	ATTGCAATAGCACGAGTTGTTTGAATGAAATGTTGCTTGGACAAGCACTGAAAGATAAG	3085
Qy	1684	CRAGACTTAAGCATGCTGGAAGATAGCAACTGAGACTTTGGAGATATACCTACTCATATA	1743
Db	3086	AAAGAACTGAAGGTGCTGGGAAGATCGCTACTTGAAGCAATAGAAAACTTCCGAACGGTT	3145
Qy	1744	GTGTCATTAACAGGGGAAAAGCCTTTCGAGCAAAATGTATGAAGAGATGCTTCAGACTCAA	1803
Db	3146	GTTCCTTTGACTCAGGAGCAGAAAGTTTGAACATATGTATGCTCAGAGTTTTCAGGTACCA	3205
Qy	1804	CRAGAAATACCTCGAAGAAAGCACAGATATTTGGAGCTGTTATGCATTCAGCCATGCC	1863
Db	3206	TACAGAAACTCTTTTGGGAAAGCACACATCTTTTGGAAATTACAATTTCTTCAACCCAGGCA	3265
Qy	1864	TTTTATATATTTTGCCCTATGCAGCAGGGTTTCGATTTTGGAGCCTATTTAAATCAAGCTGGA	1923
Db	3266	ATGATGTAATTTTCTTATGCTGATGTTTCCGGTTTTGGAGCCTACTTGTGTGGCACATAAA	3325
Qy	1924	CGAATGACCCACAGAGGCAATGTTTCATAGTTTTTACTTGCAAATTCATATGAGGCTATGGCC	1983
Db	3326	CTCATGAGCTTTGAGGATGTTCTGTAGTATTTTTCAGCTGTGTGCTTTGGTGCAATGGCC	3385
Qy	1984	ATCGGAAAAACGCTCGTTTGGCTCTCTGAATATTTCAAAGCCAAATTCGGGGGCTGCGCAT	2043
Db	3386	GTGGGCAAGTCAGATTCATTTGCTCTGACTATGCTCAAGCCAAAGCCTAAATATCAGCAGGCCAC	3445

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;SEQ ID NO:3:
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5206352-3

Query Match      36.1%; Score 1030.2; DB 6; Length 4669,
Best Local Similarity 62.2%; Pred. No. 2.5e-288;
Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;

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1526 ATAAATTGATATATAGCCAAAGTATTGCAGCTATTGGAAGTGGCCACAACCCAGATAAT 1585
226 ATAGAAGGAACCTGTGGAAATTTAAAAATGTTTCTTTCAAATTATCCCATCAAGACCATTATC 285
1586 ATTAAGGGAAATTTGGAAATTCGAATATGTTCACTTCAGTTTACCATTCTCGAAAGAAGTT 1645
286 AAGATTCGAAGAGGTCCTGAATCTCAGAAATTAAGTCTGGAGAGACAGTCGCGCTTGGTTCGGT 345
1646 AAGATCTTGAAGGCCCTGAACCTGAGAGTGCAGAGTGGGCAGACCGTGGCCCTGGTTGGA 1705
346 CTCATATGGCAGTGGGAAGAGTACGGTAGTCCAGCTCTTCGAGAGAGGTTATATGATCCGGAT 405
1706 AACAGTGGCTGTGGGAAGAGCAACAAGTCCAGCTGATGCAGAGGCTCTATGATACCCCAACA 1765
406 GATGGCTTTATCATGTGTGATGAGATGCATCAGAGCTTTTAAATGTGCGGCATATTTCGA 465
1766 GAGGGGATGGTCAGTGTGATGGACAGGATATTAGGACCATAAATGTAAAGTTTCTACGG 1825
466 GACCATATTGGAAGTGTGTAGTCAAGAGCTGTTTGTTCGGACCAACCATCAGTAACAT 525
1826 GAAATCAITTGGTGTGGTGAAGTCAAGGAACCTGTATTGTTTGGCCACCAGTAGCTGAAAC 1885
526 ATCAAGTATGGAACAGATCATGTGACTGATGAAGAGATGGAGAGAGCAGCAAGGGGAAGCA 585
1886 AITTCGCTATGGCCGTGAAATGTCAACATGGATGAGATTGGAAAGCTGTCAAGGAAGCC 1945
586 AATGCGTATGATTTTATTCATGGAGTTTCTTAATAAATTTAATATCATTGGTAGGGAAATA 645
1946 AATGCGTATGACTTTATCATGAAGAACTGCCCTCAATAAATTTTGACACCCCTGGTTGAGAGAGA 2005
646 GGAGCTCAAAATGAGTGGAGGGCAGAAACAGAGGATCGCAATTGTCTGCGCTTAGTTTCGA 705
2006 GGGGCCCACTTGAGTGTGGCAGAGCAGAGGATCGCCATTGCACGTGCGCTGGTTGCG 2065
706 AACCCTCAAGATTCGATTTTATGATGAGGCTAAGTCTGCCCTGGATTTCAGAAAGCAAGTCA 765
2066 AACCCTCAAGATCCTCTGCTGATGATGGCCAGTCAAGCTCAGCTGACAGCAAGACGGAGCA 2125
766 GCTGTTCAAGCTGCATCTGAGAGAGCGCAGCAAGGTCGGAGCTCAATCTGTTGGTAGCACAC 825
2126 GTGTTTCAGTGGCTCTGATGAGGCCAGAAAAGGTCGGACCACCACTTGTGATAGCTCAT 2185
826 CGACTTCTTACTATTTCGAAGTCCAGATTTGATTTGACCCCTAAAGATGGATGCTGGCG 885
2186 CGTTGTGCTACAGTTCGTAAATGCTGACGTGATCGCTGGTTCGATGATGAGTCAATTGTG 2245
886 GAGAAAGGAGCAGATCTCTGAACTAATATGGCAAAACGAGGCTCTATATTATTCACTTGTGATG 945
2246 GAGAAAGGAATCATGATCAACTCATGAAAGAGAAAGGCATTTACTTCAAACCTGTTCACA 2305
946 TCAAGGATATTAAAAAGCTGATGAACAGATGGAGTCAATGATCATATGATCATATTCTA 997
2306 ATGCAGACAGCAGGAAATGAAGTTGAATTAGAAAATGCAAGTCTGATGAAATCCAAAAGTGA 2365
998 -----CTGAAAAGAAAGACCAACTCACTTCTCTCTGCACTCTGTGGAAGAGCATCA--- 1045
2366 ATTGATGCTTGGAATGTCTTCAAATGATTCGAAGATCCAGTCCAGTCTAATTAAGAAAAGATCA 2425
1046 -----AGTCAGACTTCATTGACAAGGCTGAGGAATCCACCCCAATCT 1086
2426 ACTGTAGGAGTGTCCGTGGATCAAGGCCACAGACAGAAAGCTTAGTACCAAGAGGCT 2485
1087 AAAGAGATAAGTCTTCCCTGAAGTCTCTTATTAATAAATTTTAAAGTTTAAACAAGCCTGAA 1146

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[illegible]

PRIOR APPLICATION DATA:					
APPLICATION NUMBER: DE P 44 31 973.8					
FILING DATE: 08-SEP-1994					
PRIOR APPLICATION DATA:					
APPLICATION NUMBER: DE 195 03 952.1					
FILING DATE: 07-FEB-1995					
PRIOR APPLICATION DATA:					
APPLICATION NUMBER: PCT/EP95/03175					
FILING DATE: 10-AUG-1995					
ATTORNEY/AGENT INFORMATION:					
NAME: Berman, Richard J.					
REGISTRATION NUMBER: 39,105					
REFERENCE/DOCKET NUMBER: P1614-7007					
TELECOMMUNICATION INFORMATION:					
TELEPHONE: (202)638-5000					
TELEFAX: (202)638-4810					
INFORMATION FOR SEQ ID NO: 5:					
SEQUENCE CHARACTERISTICS:					
LENGTH: 6505 base pairs					
TYPE: nucleic acid					
STRANDEDNESS: double					
TOPOLOGY: circular					
MOLECULE TYPE: DNA					
US-08-793-610-5					
Query Match 36.1%; Score 1030.2; DB 2; Length 6505;					
Best Local Similarity 62.2%; P-ed. No. 3e-288;					
Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;					
QY	166	ATTTGATAGAAACCCAGTATGATTAATTCCTCAAGTGTGGTGAATTC	225		
DB	2918	ATAAATTTGATAAAGAACAAGTATTCAGAGCTATTCGAAGAGTGCGGCACAAACCAGATAAT	2977		
QY	226	ATAGAAGGAACCTGTGGAATTTAAAATGTTTTTCAATTAATCCTCAAGACCATCATC	285		
DB	2978	ATTAAGGAAATTTGGAATTCAGAAATGTTTCACTTCAGTTACCCATCTCGAAGAAGATT	3037		
QY	286	AAGATTCTCAAAGGTCTGAATCTCAGAAATTAAGTCTGAGAGACAGTGGCTTGGTGGGT	345		
DB	3038	AAGATTCTCAAAGGTCTGAATCTCAGAAATTAAGTCTGAGAGACAGTGGCTTGGTGGGT	3097		
QY	346	CTCAATGGCAGTGGGAAGTAGCTAGTCCAGCTTCTGCAAGGTTATATGATCCGGAT	405		
DB	3098	ACAGTGGCTGTGGGAAGACGACACAGTCCAGCTGATGCGAGGCTCTATGACCCACCA	3157		
QY	406	GATGGCTTTATCATGTGTGATGAGAAATGACATCAGAGCTTTAAATGTGCGGCATTATCGA	465		
DB	3158	GAGGGATGCTCAGTGTTCATGACAGAGGATATTAGAACCAATAATGTAAGGTTTTCACGG	3217		
QY	466	GACCATATTGAGTGTGTAGTCAAGACCTGTTTGTTCGGGACCAACATCAGTAAACAAT	525		
DB	3218	GAAATCATTTGGTGTGTAGTCAAGAACTGTATTGTTTGGCCACACGATAGCTGNAAAC	3277		
QY	526	ATCAAGTATGACGAGATCATGTACTGATGAAGAGATGAGAGACAGCAGCAAGGGAAGCA	585		
DB	3278	ATTGCTATGGCGTGAAATGTCCACATGGATGAGATTGAGAAGCTGTCAAGGAGGCC	3337		
QY	586	AATGCTATGATTTTATCATGAGTTTCTTAATAAATTTATATCATTTGTTAGGGGAAAAA	645		
DB	3338	AATGCTATGATTTTATCATGAGTTTCTTAATAAATTTATATCATTTGTTAGGGGAAAAA	3397		
QY	646	GGAGCTCAATGATGAGGAGGAGCAAGAGGATGCGCAATTCCTGCTGCTTATGTTTCCA	705		
DB	3398	GGGGCCCGTTGAGTGGTGGGAGAGAGAGATTCGCCATTCACGTCGCTGCTGCTGCTG	3457		
QY	706	AACCCCAGATTTCTGATTTTATGATGAGGCTACGTTGCCCTCGATTCAGAAAGCAAGTCA	765		
DB	3458	AACCCCAGATTTCTGATTTTATGATGAGGCTACGTTGCCCTCGATTCAGAAAGCAAGTCA	3517		
QY	766	GCTGTTTCAGCTGCATCTGAGAGGCGCACCAAGCTCGACTACAACTCGTGTGAGCACAC	825		
DB	3518	GTGGTTCAGGCTCTGATTAAGGCGCAGAAAGGTCGACCAACCATTTGATAGCTCAT	3577		

4658 ATGATGATATTTCTTCTATGCTGATGTTTCCGTTTGGAGCCTACTTGGTGCCATATA 4717
1924 CGAATGACCCAGAGGCGATGTTTACTGCAATTCATATGAGCTATGCGC 1983
4718 CTCATGAGCTTGGAGATGTTCTGTTAGTATTTTCAGCTGTTGTTGTCCTATGCC 4777
1984 ATCGGAAACGCTGTTTGGCTCTGTAATATTCGAAAGCAATTCGGGGGCTCGCAT 2043
4778 GTGGGCAAGTCAGTTTCTGCTGCTGATGCTGCAAGCAAGCAAGCAAGCAAGCAAG 4837
2044 CTGTTTGCCTTGTGAAAGAAACCAATATAGACAGCGCGAGTCAAGAGGGAAGAAAG 2103
4838 ATCATCATGATCATTTGAAAGAACCTTTGATGACAGTACAGACGGAAGCCTATG 4897
2104 CCAGACATGTAAGGGAATTTAGAGTTTCGAGAGTCTTCTTCTTATCCATGTCGC 2163
4898 CCGAACATTCGAAGGAATGTCATTTGTTGAGTTGTTTCACTATATCCACCCGGA 4957
2164 CCAGATGTTTTCATCTCTCGTCTGTTTCTGCTGATGTTGAGCGGGAAGCACTAGCA 2223
4958 CCGACATCCGAGTGTCTCAGGACTGAGCCTGAGGTGAGAGGCGGAGCGTGGCT 5017
2224 TTTTGGGAGCAGCGGCTGTGGGAAAGCACTTCTGTTCACTTCTGAGAGACTTTAT 2283
5018 CTGTTGGCAGCAGTGTGCTGTGGAGAGCAGAGTGTCCAGCTCTGAGCGGTTCTAC 5077
2284 GACCCGTCGAGGACAGTGTCTGTTGAGTGTGATGCAAGAAATGATGATGATGATG 2343
5078 GACCCCTTGGCAGGGAAGTGTGCTGTTGATGCAAGAAATGATGATGATGATGATG 5137
2344 TGCTCTCGTTCCCAATAGCAATCGTTCTCTCAAGAGCCTGCTCTTCACTGCAAGCAT 2403
5138 TGCTCTCGAGACACCTCGGCTGCTGCTCCAGAGGCGCATCTGTTGACCTGAGCAT 5197
2404 GCTGAGACATGCTTATGTCAGACAGCGCTGTTGTCGATGATGATGATGATGATGATG 2463
5198 GCTGAGACATGCTTATGTCAGACAGCGCTGTTGTCGATGATGATGATGATGATG 5257
2464 GCGCAATGTCAGCAATATCAATCTTCTTATGAGGCTCTCCCTGAGAAATACAAACA 2523
5258 GAGCAAGAGGCGCACTATGATGATGATGATGATGATGATGATGATGATGATGATG 5317
2524 CAATTTGAGTGAAGGAGCAGCTTCTGTCGCGCCGAGAAACAAAGACTAGCTATTGCA 2583
5318 AAAGTAGGAGACAAAGGAATCAGCTCTCTGTCGCGCCAGAAACAAAGCAAGCAAG 5377
2584 AGGCTCTTCTCCAAAGCCCAATTTTATGTTGATGAGGCGCACTTCAGCCCTCGAT 2643
5378 CGTGCCTTGTGATGAGCAGCTCTATATTTTCTTTTGGATGAGGCGCACTCTGAT 5437
2644 AATGACAGTGAAGAGTGTGTCAGCATGCCCTTGTGATAAGCCAGGAGGAGGAGCATGC 2703
5438 ACAGAAAGTGAAGAGTGTGTCAGAAAGCCCTGGACAAAGCCAGAGAGGCGCACCTGC 5497
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5498 ATTGTGATTTCTCAGCGCTCTGCAATTCAGAAATGCAAGTGAATGATGATGATGATG 5557
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2824 TTTAAGTTAGTGAATGCAAGTCAAG 2848
5618 TTTTCAATGTCAGTGTCCAGGCTG 5642

RESULT 6
US-08-793-610-6
; Sequence 6, Application US/08793610
; Patent No. 5858744
; GENERAL INFORMATION:

APPLICANT: BAUM, Christopher
APPLICANT: STOCKING-HARRIS, Carol
APPLICANT: OSTERTAG, Wolfram
TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
TITLE OF INVENTION: FOR GENE TRANSFER
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,610
FILING DATE: 07-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 31 973.8
FILING DATE: 08-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03175
FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berman, Richard J.
REGISTRATION NUMBER: 39,105
REFERENCE/DOCKET NUMBER: P1614-7007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9318 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-08-793-610-6
Query Match 36.1%; Score 1030.2; DB 2; Length 9318;
Best Local Similarity 62.2%; Pred. No. 3.7e-288;
Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;
QY 166 ATTATTGATTAAGAAACCCAGTATAGATACTTTTCCACAGCTGGATTAACCTGATCC 225
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DB 2937 ATTAAGGAAATTTGGAATTCAGAAATGTTCACTTCAGTACCATCTCGAAAGAAAGATT 2996
QY 286 AAGATTCTGAAGGCTCTGAATCTCAGAAATTAAGTCTCGAGAGACAGTGGCTTGGTGGT 345
DB 2997 AAGATCTTGAAGGCTCTGAATCTCAGAAATTAAGTCTCGAGAGACAGTGGCTTGGTGGT 3056
QY 346 CTCAATGCGAGTGGAGAGTACCGTATGCTGAGCTTCTGCAAGGTTATATGATCCGAT 405
DB 3057 AACAGTGGCTGTGGAGAGAGACCAACAGTCCAGTGTATGCAAGAGCTCTATGACCCCA 3116
QY 406 GATGCTTTTATCATGCTGGATGAGATGACATCAGAGCTTTTAAATGTGCGGCATTTATCGA 465
DB 3117 GAGGGATGCTCAGTGTGATGGACAGGATATTAGGACCAATAAATGTAAGGTTTCTACGG 3176
QY 466 GACCATATTGAGTGGTGTAGTCAAGAGCTGTTTGTTCGGGACCAACCATCAGTAACAT 525
DB 3177 GAAATCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 3236

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4317		1624	CTTGGCGTGACAGGAATGATTTGAACCCGACGCAATGACATGGATTTTGGCAACAAAGATAAG
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4377		1684	CAAGAACTTAAGCATGCTTGGAAAGATAGCAACTGAAAGCTTTGGAGNATATAGTACTATA
1684		4437	AAAGAACTAGAGGTGCTCTGGAGATCGCTACTCTGAAGCAATAGAAAACTTTCCGAACCGTT
4437		1744	GTGTCATTTAAACAAGGGAAAAGCCCTTCAGACGAAATGTTATGAAGAGATGCTTCAGACCTCAA
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4496		1803	CACAGAAATACCTCGAAGAAAGCACAGATATTTTGAGAGCTGTTATGCAATTCAGCCTATGCC
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4557		1864	TTTATATATTTTCCCTATGACAGCAGGGTTTCGATTTGGAGCCCTATTAAATTCAGCTGGA
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1984		4737	GTGGGCGAAGTCAGTTCATTTTCTCTGCTACTATGCCAAAGCCAAATATCAGCAGCCAC
4737		2044	CTGTTTGCCTTGTGGAAGAGAAAACMAATATAGACAGCGGAGTCACAGNAGGGAAGAAAG
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4857		2164	CCAGATGTTTTCACTCTCGTGGCTTATCCCTCAGTATTGAGCGAGGAAGACAGTAGCA
2164		4917	CCGGAATCCCATGCTTTCAGGCACTGAGCCTCGAGGTGAAAGAGGCCACAGACCTGGCT
4917		2224	TTTGTGGGAGCAGCGCTGTGGGAAAAGCACTTCTGTTCAACTTCTTCGACAGACTTTAT
2224		4977	CTGTTGGCGCAGCAGTCTGTTGATGGTGATGATGCAAAAGTAATGTAATGTACAG
4977		2284	GACCCCGTGAAGGACAGTCTGTTGATGGTGATGATGCAAAAGTAATGTAATGTACAG
2284		5037	GACCCCTGGCAGGGAAAGTGCTCTGTATGTCGCAAAAGAAATAAGCGACTGAATGTTTCAG
5037		2344	TGCTCCGTTCCCAATAGCAATTCGTTCTCTCAAGAGCCTGTGCTCTTTCAACTGCAGCAT
2344		5097	TGGCTCCGAGGACACCTGGGSCATCGTGTCAGAGAGCCCATCTCTGTTGACTGCAGCAT
5097		2404	GCTGAGAAATCCCTATGGTGAACACAGCCGTGTGGTGCCATTAGATGATGATCAAGAA
2404		5157	GCTGAGAAATTCCTTATGGAGAACAAGCCCGGTGGTGTCACAGGAAGAGATCGTAGG
5157		2464	GCCCAATTCAGCAAAATATCCAATCTTTTATTTGAAGGTTCCCTCGTGAAGAAATACACACA
2464		5217	GCAGCAAGAGGCCCAACATACATGCTTCCATCGAGTCACTGCTCCTAATAATATAGCACT
5217		2524	CAAGTTGGAAGAGGACAGACTTTCTGGGGCCGACAGAAACAAGACTAGCTATTGCA
2524		5277	AAAGTAGGACAAAGGAACTCAGCTCTCTGGTGGCCAGAAAAAACGCATTCGCCATAGCT
5277		2584	AGGGCTCTTCTCCAAAAAACCAGAAATTTTATTTGATGAGGCGCACTTCAGCCCTCGAT
2584		5337	CGTGCCCTCTGTAGACAGCTCATATTTTGTCTTTTGGATGAGGCCAAGCCAGCTCTGGAT
5337		2643	CGTGGCTCTGTTAGACAGCTCATATTTTGTCTTTTGGATGAGGCCAAGCCAGCTCTGGAT
2643		5396	CGTGGCTCTGTTAGACAGCTCATATTTTGTCTTTTGGATGAGGCCAAGCCAGCTCTGGAT
5396		2703	CGTGGCTCTGTTAGACAGCTCATATTTTGTCTTTTGGATGAGGCCAAGCCAGCTCTGGAT

Db 5397 ACAGAAAGTGAAGAGTTGTCAGAGAGCCCTGGACAAAGCCAGAGAGAGCCGACCTGC 5456
Qy 2704 CTAGTGGTCACTCACAGGCTCTCTGCAATTTCAGAACGCGAGATTGATAGTGTCTGAC 2763
Db 5457 ATTGTGATGCTCACCGCTGTCCACCATCCAGAAATGCAGACTTAATAGTGTGTTTCAG 5516
Qy 2764 AATGGAAGATAAGCAACAGCAATCTCATCAGAGCTCCTCGAATCGAGACATATAT 2823
Db 5517 AATGGCAGAGTCAGAGAGATGCGACGATCAGCAGTCTGCTGGCAGAAAGGCATCTAT 5576
Qy 2824 TTAAAGTTAGTGAATCACAGTCAG 2848
Db 5577 TTTTCAATGGTCAGTGTCCAGGCTG 5601

RESULT 7
US-08-784-649A-1
; Sequence 1, Application US/08784649A
; Patent No. 5830697
; GENERAL INFORMATION:
; APPLICANT: Sikic, Branimir I
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
; TITLE OF INVENTION: CYCLOSPORIN MODULATION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,649A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: Reg.No. 5830697 36,677
; REFERENCE/DOCKET NUMBER: 06037/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4264 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-784-649A-1

Query Match 36.0%; Score 1028.6; DB 2; Length 4264;
Best Local Similarity 62.2%; Pred.No. 6.9e-288;
Matches 1694; Conservative 0; Mismatches 989; Indels 42; Gaps 3;

Qy 166 ATTATTGATGAAGAACCCAGTATAGATAACTTTTCCACAGCTGATATATAACCTGATCC 225
Db 1240 ATAATTGATATAGCCAGATTTTGACAGCTATTTCGAGAGTGGGCAACACAGATAAT 1299
Qy 226 ATAGAAGGAAGCTGGGAATTTAAATAATGTTTCTTCAATTATTCATCAAGACCATCTATC 285
Db 1300 ATTAAGGGAATTTGGAATTCAGAAATGTTTCACTTCAGTTACCCATCTCGAAAAGAGTT 1359
Qy 286 AAGATTCGAAAGCTCTGAATCTCAGAAATTAAGTCTCGAGAGCAGTCGCTGTCGGT 345
Db 1360 AAGATCTGAAGGCGCTGAACCTCAAGGTGCAAGTGGGCGACGCTGGCCCTGGTTGGA 1419

Qy 346 CTCATGCGAGTGGGAAGAGTACGGTAGTCCAGCTTCTGCGAGAGTTATATGATCCGGAT 405
Db 1420 AACAGTGGCTGTGGGAAGAGCAACAGTCCAGCTGATGCGAGAGCTCTATGACCCCA 1479
Qy 406 GATGCTTTTATCATGTGGATGAGAAATGACATGAGAGCTTTAAATGTGCGCATTTATCGA 465
Db 1480 GAGGGATGGTCACTGTTGATGGAAGAGATATTAGGACCAATAAATGTAGGTTTCTAOG 1539
Qy 466 GACCATATTTGAGTGGTTAGTCAAGAGCTGTTTGTTCGGGACCAACCATCAGTAACAA 525
Db 1540 GAATCATTTGGTGGTGGTCAAGAACCTGTATTGTTTGGCCACCAAGATAGTCAAAAC 1599
Qy 526 ATCAAGTATGACGAGATGATGTGACTGATGAAGAGATGGAGAGAGAGCAAGGAAAGCA 585
Db 1600 ATTGCTATGGCGGTGAATAATGTCAACATGATGAGATTGAGAAAGCTGTCAAGAGGCC 1659
Qy 586 AATGCGTATGATTTATCATGAGTTCCTTAATAAATTAATACATTTGTTGGGAAAAA 645
Db 1660 AATGCTATGACTTTATCATGAACCTGCTCATAAATTTGACACCCCTGGTGGAGAGAG 1719
Qy 646 GGAGCTCAATGAGTGGAGGCGAGAAACAGAGGATGCGCAATTGCTGTCGCCCTTACTGCA 705
Db 1720 GGGGCCAGTTGAGTGGTGGCGAGAGCAGAGGATGCGCAATTGACAGTGCCTGTTGCG 1779
Qy 706 AACCCCAAGATTTCTGATTTTATGATGAGGTAGTCTGCTCCCTGGATTCAGAAAGCAAGTCA 765
Db 1780 AACCCCAAGATCTCTCTGCTGATGAGGCGCAGCTCAGCCTTTGGACACAGAAAGCGAAGCA 1839
Qy 766 GCTGTTCAAGCTGCACTGAGAGGCGAGCAAGGTGCGACTTACAAATCGTGTGTAGCACAC 825
Db 1840 GTGGTTCAAGTGGCTCTGATGAAGCCAGAAAGGTGCGACCCATTTGTGATAGTCTCAT 1899
Qy 826 CGACTTTCTACTATTGCGAAGTGCAGATTTGATTTGTGACCTTAAGAGATGGAATGCTGGG 885
Db 1900 CGTTTGTCTACAGTTGCTAATGCTCAOGTCACTGCTGGTGTTCGATGATGAGGAGCTATTGTG 1959
Qy 886 GAGAAAGGAGCACATGCTGACTAATGCGCAAGAGGCTCTATATTTTCACTTTGTGATG 945
Db 1960 GAGAAAGGAAATCATGATGACTCATGAAGAGAAAGGCTTTACTTCAATTTGTGCACA 2019
Qy 946 TCACAGGATATTAAAGAGCTGATGAACAGATGAGTGCATGACATATTTCTA----- 997
Db 2020 ATGCAGACAGCAGGAAATGAAGTTGAATTAGAAATGCAGCTGATGAATCCAAAGTGAA 2079
Qy 998 -----CTGAAAGAAAGACCAACTCACTTCCTCTGCACTCTGTGAGAGCATCA--- 1045
Db 2080 ATTGATGCGCTTGGCAATGTCTTCAAAATGATTCAGAGTCCAGTCTTAATAGAAAAGATCA 2139
Qy 1046 -----AGTCAGACTTCAATTGACAAGGCTGAGGAATCCACCCCAATCT 1086
Db 2140 ACTCGTAGAGTGTCCGTGGATCAACAAGCCCAAGACAGAAAGCTTAGTACCAAGAGGCT 2199
Qy 1087 AAAGAGATAAGTCTTCTGAGTCTCTCTATTAAATAATTTTAAAGTTTAAAGTTAAACAGCTGAA 1146
Db 2200 CTGATGAAGATATACCTCCAGTTTCTTCTTGGAGATTTATGAAGCTAAATTTAACTGAA 2259
Qy 1147 TGGCCTTTTGTGGTTCTGGGAGACATTTGGCTTCTGTTCTAAATGGAACCTGTTTCATCCAGTA 1206
Db 2260 TGGCCTTATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2319
Qy 1207 TTTTCATCATCTTTGCAAAAATTAACCATGTTTGGAAATTAATGATATAAACCAATTA 1266
Db 2320 TTTGCAATAATATTTTCAAGATTTATAGGGGTTTTTACAGAAATGATGATCTCTGAAACA 2379
Qy 1267 AAG---CATGATGACAGAAATTTTATCCATGATTTGCTCATTTTGGGTGTTATTGCTTT 1323
Db 2380 AAAGCAGAAATAGTAACTTGTGTTTTCATTTGTTTCTAGCCCTTGGAAATTTATTTCTTT 2439
Qy 1324 GTCAGTTATTTTCAGAGGATTTATTTTACGCGAGAGGAGGAAATTTTACGATGAGA 1383
Db 2440 ATTACATTTTTTCTTCAGGGTTTTCATTTTGGCAAAGCTGGAGAGATCCTTCAACAAGCG 2499

3580 GCAGCAAGGAGGCCAACATACATGCTTTCATCGAGTCACTGCTTAATAAATATAGCACT 3639

2524 CAAGTTGGACTCAAGAGGACACAGCTTCTTGGGGGCCAGAAACAAAGACTAGCTATTGCA 2583

3640 AAGTAGAGAGACAAAGAACTAGCTCTCTGTGGCCAGAAACAAACGATGGCCTAGCT 3699

2584 AGGGCTCTTCTCAAAAAACCCAAATTTATTTGTTGGATGAGGCCACTTCAGCCCTCGAT 2643

3700 CGTGCCCTTGTAGACAGCGCTCATATTTTGTCTTTTGGATGAAGCCAGCTCAGCTCTGGAT 3759

2644 AATGACAGTGAAGGTGTTTCAGCATGCCCTTGATAAAGCCAGGACGGCAAGACATGC 2703

3760 ACAGAAAGTGAAGGTGTTCCAGAGAGCCCTGGACAAAGCCAGAGAGCGCCGACCTGC 3819

2704 CTATGGTCACTACACAGGCTCTCTGCAATTCAGAACGCGAGATTTGATGTTCTGCAC 2763

3820 ATTGTGATTGCTCACCGCTGTCCACCATCCAGAAATGCGAGACTTAATAGTGTGTTTCAG 3879

2764 AATGAAAGATAAGCAACAGCAAGCACTCATCAGAGCTCCTGAGAAATCGAGACATATAT 2823

3880 AATGGCAGAGTCAAGAGCATGCGACGATCAGCAGCTGCTGGCACAGAAAGCATCTAT 3939

2824 TTTAAGTTAGTGAATGCACAGTCAG 2848

3940 TTTTCAATGTCAGTGTCCAGGCTG 3964

RESULT 8

US-08-784-649A-5

Sequence 5, Application US/08784649A

Patent No. 5830697

GENERAL INFORMATION:

APPLICANT: Siskic, Branimir I

APPLICANT: Chen, Gang

TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO

TITLE OF INVENTION: CYCLOSPORIN MODULATION

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSER: Fish & Richardson

STREET: 2200 Sand Hill Road

CITY: Menlo Park

STATE: CA

COUNTRY: USA

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/784,649A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Sherwood, Pamela J

REGISTRATION NUMBER: Reg.No. 5830697 36,677

REFERENCE/DOCKET NUMBER: 06037/007001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-322-5070

TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 4264 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-784-649A-5

Query Match 36.0%; Score 1028.6; DB 2; Length 4264;

Best Local Similarity 62.2%; Pred.No. 6.9e-288;

Matches 1694; Conservative 0; Mismatches 989; Indels 42; Gaps 3;

166 ATATTGATAAGAAACCCAGTATAGATATCTTTCCACAGCTGATATTAACCTGATCC 225
1240 ATAAATGATTAAGCCCAAGTATTCACAGCTATTTGGAAGAGTGGGCAAAACAGATAT 1299
226 ATAGAAGGAATCTGGGAATTTAAATATTTCTTTCAATTTATTCATCAAGACCATCTATC 285
1300 ATTAAGGGAAATTTGGAAATTCAGAAATGTTCACTTCAGTTACCCATCTCGAAAAGAGTT 1359
286 AAGATTTCTGAAGGCTCTGAATCTCAGAAATTAAGTCTCGAGAGACAGTGCCTTGGTCGGT 345
1360 AAGATTTGAAGGCCCTGAACCTGAAGCTGAGAGTGGGAGACGGTGGCCCTGGTTGGA 1419
346 CTCAATGGCAGTGGGAAGAGTACGGTAGTCCAGCTTCTCGAGAGGTTTATATGATCCGGAT 405
1420 AACAGTGGCTGTGGGAAGAGCACAACAGTCCAGCTGATGAGAGGCTCTATGACCCCA 1479
406 GATGGCTTTATCATGGTGGATGAGAAATGACATCAGAGCTTTAAATGTGGGCAATATCGA 465
1480 GAGGGAGTGTGAGTGTGATGAGCAGGATATTAGGACCAATAAATGTAAGGTTTCTACGG 1539
466 GACCATAATGAGTGGTGTAGTCAAGAGCTGTTTGTTCGGGACCAACCATCAGTAACAT 525
1540 GAATCATTTGTGTGGTGTGAGTCAAGAGCTGTATTGTTTCCACACGATAGCTGAATC 1599
526 ATCAAGTATGGAAGAGATGATGTGATGATGAGAGATGAGAGAGAGCAGCAGAGGAGCA 585
1600 ATTGCTATGGCCGTGGAATGTCAACATGATGAGATTCAGAAAGCTGTCAAGAGAGCC 1659
586 AATCGGTATGATTTATCATGAGTGTTCCTAAATAATTTAAATACATTTGATGGGAAAA 645
1660 AATGCTATGATCTTTATCATGAACTGCTCTCATTAATTTGACACCTGGTGTGAGAGAG 1719
646 GGAGCTCAAAATGAGTGGAGGCGAGAAACAGAGGATCGCAATTCGTGCTTGTAGTTCGA 705
1720 GGGGCCAGTTGAGTGTGGGAGAGCAGAGGATCGCAATTCGACGCTGCTGCTGCTGCTG 1779
706 AACCCAGAGATTCATGATTTAGTATGAGCTACGTTGCTGCTGCTGCTGCTGCTGCTGCTG 765
1780 AACCCAGAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1839
766 GCTGTTCAAGCTGACATCGGAGAGCGAGCAAGGTCGGACTACAAATCTGTGGTAGCACAC 825
1840 GTGGTTCAAGTGGCTCTGATATGAGCCAGAAAGTCCGACCCCAATTTGTGATGCTCAT 1899
826 CGACTTTCTACTATTGCAAGTGCAGATTTGATTTGTGACCTTAAGATGGAATGCTGGCG 885
1900 CGTTTGTCTACGTTCTGATTAAGTGTGACCTCATGCTGCTGCTGCTGCTGCTGCTGCTG 1959
886 GAGAAAGAGCACATGCTGAACATAATGGCAAAACAGGCTCTATATTTCACTTGTGATG 945
1960 GAGAAAGGAATCATGATGAATCATGAGAGAGAAAGGCAATTTACTTCAAACTTGTACA 2019
946 TCACAGGATATTAAGAAAGCTGATGAACAGATGAGTCAATGACATTTCTA----- 997
2020 ATGCAGACAGCAGGAAATGAGTTGAATTAAGAAATGCAAGTCAATGAAATCCAAAGTGAA 2079
998 -----CTGAAGAAAGAACCAACTCCTCTGCACTCTGCAAGAGCATCA--- 1045
2080 ATTGATGCTTGGAAATGCTTCAATATGATTCAGATCCAGTCTAATTAAGAAAGATCA 2139
1046 -----AGTCAGATTCATTGCAAGGCTGAGGAATCCACCCATCT 1086
2140 ACTGATGAGTGTCCGTGGATCAAGCCCAAGACAGAAAGCTTAGTACCAAGAGGCT 2199
1087 AAGAGATAGTCTTCTGAGTCTCTTATTAATAATTTTAAGTTTAAACAGCCCTGAA 1146
2200 CTGATGAAGAGTATACCTCCAGTTTCTTTTGGAGGATTAAGAGCTAAATTTAACTGAA 2259
1147 TGGCCTTTGTGGTCTGGGACATGCTTCTGTTCTTAATGGAATGTTTCAATCCAGTA 1206
2260 TGGCCTTTATTTGTGTGTGTTATTTGTGCTGATGCTGCAAAAGATTTGAATGTACAG 2319

1207 TTTTCATCATCTTTGCAAAAATTTATACCATGTTTGGAAATAATCATATAAACCAATTA 1266
2320 TTTGCAATATATTTTCAAGATTTAGGGGTTTTTACAAGAAATTCATGATGATCTGAAACA 2379
1267 AAG---CATGATGACAGAAATTTATTCATGATATTCGTTCATTTTGGGTGTTATTTCTTT 1323
2380 AAAACGACAGATAGTAACCTTTGTTTTCATTAATTTCTAGCCCTTGGAAATTTATTTCTTT 2439
1324 GTCAGTTATTTCAATGACAGGATTTATTTACGGCAGACAGGAGAAATTTTAAACGATGAGA 1383
2440 ATTACATTTTCTTCAAGGTTTTCATTTGGCAAGCTGGAGAGATCCTCACCAGGCG 2499
1384 TTAAGACATCTGGCCTTCAAGCCATGTTTATATCAGGATATTTCCCTGGTTTGAATGAAGA 1443
2500 CTCGATATCATGTTTTCGATCCATGCTCAGACAGGATGTGAGTTGGTTTGTATGACCCCT 2559
1444 GAAAACAGACACAGGAGGCTTGAACAATATTAGCCATAGATATATGACAAATTTCAAGCA 1503
2560 AAAAAACACCTGAGCATTTGACTACAGCTCGCAATGATGCTGCTCAAGTTAAAGG 2619
1504 GCAACAGGTTCCAGGATGGCGTCTTAAACAAAAATGCAAAATGCAAAATGGGACTTTTCA 1563
2620 GCTATAGTTCCAGGCTTCTGTAATTAACCCAGATATAGCAAAATCTTGGACAGGAATA 2679
1564 ATCATTTCTTTATATATGATGGGAGATGACATCTCTGATTTCTGAGTATGCTCCAGTA 1623
2680 ATTATATCTTCTCATCTATGTTGGCAACTTAACATCTTTACTCTTAGCAATTTGATCCATC 2739
1624 CTTCGCTGACAGGATGATTTGAAACCGCAGCAATGACTGGATTTTCCCAACAAAGATAAG 1683
2740 ATTGCAATAGCAGGAGTCTGTTGAAATGAAATGTTGTTCTGGAACAACACTGAAAGATAAG 2799
1684 CAAGAACTTAAGATGCTGGAAGATAGCACTGAAGCTTTGGAGATATATGATCTATA 1743
2800 AAGAACTAAGAGGTTGCGGAAGATCGCTACTGAAGCAATAGAAATCTTCGACCGTT 2859
1744 GTGCTAATAACAGGAAAAAGCCTTCGAGCAAAATGATGAAGAGATGCTTCAGACTCAA 1803
2860 GTTCTTTGACTCAGGAGCAGAGTTTGAACATATGATGCTCAGAGTTTGCAGSTPACCA 2919
1804 CACAGAAATACCTCGAAGAAAGACAGATTAATGGAAGCTGTTATGCAATTCAGCCTATGCC 1863
2920 TACAGAACTCTTTGAGGAAAGCACATCTTTGGAATTTACATTTTCTTCCACCCAGCA 2979
1864 TTTATATATTTTCTGCTATGACAGGCTTTTCGATTTGGAGCTTATTTAATTTCAAGCTGGA 1923
2980 ATGATGATTTTCTTCTGCTGATGTTTCCGTTTGGAGCTTACTTGTGTGCAATATAA 3039
1924 CGAATGACCCCGAGAGGCAATGTTCAATGTTTTCATGCAATTTGCAATGAGCTATGGCC 1983
3040 CTCATGAGCTTTGAGGATGTTCTGTTAGTATTTTCAAGCTGTTGCTTTGCTGCTGCTGCTG 3099
1984 ATCGGAAACCGCTCGTTTGGCTCTGAAATTTCCAAAGCCAAATCGGGGCTGCGCAT 2043
3100 GTGGGCAAGTCAGTTTCAATTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3159
2044 CTGTTTGCCTTTGTTGAAAAAGAAACCAATATAGACAGCGCAGCTCAAGAAAGGAAAAAG 2103
3160 ATCATCATGATCATTTGAAAAAACCCCTTTTGAATGACAGCTACAGCACGGAAGGCTTAATG 3219
2104 CAGACACATGTGAAGGAAATTTAGAGTTTTCAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCT 2163
3220 CCGAACACATTTGGAAGAAATGTCATTTGTTGAGGTTGTTATTTCAACTATTTCCACCCGA 3279
2164 CAGATGTTTCTCATCTCTCGTGGCTTATCTCTCAGTATTTGAGCGAGGAAAGACAGTAGCA 2223
3280 CCGGACATCCAGTGTCTTCAAGGATGAGCTGAGGCTGGAAGGAGGCGCAGAGCTGGCT 3339
2224 TTTGTGGGAGCAGCGGCTGTGGGAAAAAGCACTTCTGTTCAACTTCTGAGAGACTTTAT 2283
3340 CTGGTGGGAGCAGTGGCTGTGGGAAAGCAGAGTGGTCCAGCTCTCGAGGCGTTCTAC 3399
2284 GACCCCGTCAAGGACAAGTGTGTTTGTGATGTTGTTGATGCTGCAAAAGATTTGAATGTACAG 2343

Db 3400 GACCCCTGGCAGGGAAGTCTCTCTGATGGCAAGAAATAAAGCGACTGAATGTTGAG 3459
Qy 2344 TGGCTCCGTTCCCAAAATAGCAATCGTTCTCAAGAGCGCTGTGCTTTCAACTGCGAGCAT 2403
Db 3460 TGGCTCCGAGCACACCTGGGCATCGTCTCCAGAGCCCATCTCTGTTGCTGCGAGCAT 3519
Qy 2404 GCTGAGACATCGCTATGTTGCAACAGCGCTGTGCTGCTTATGATGAGATCAAGAA 2463
Db 3520 GCTGAGAACATGCTCTATGAGAACAGACCGGCTGTGCTACAGGAGAGATGTTGAGG 3579
Qy 2464 GCCCAATGAGCAAAATATCATTTCTTTTATTTGAAGGCTCTCCCTGAGAAATACACACA 2523
Db 3580 GCAGAAAGGAGGCCAACATACATGCTTCTATCGAGTCAGTGGCTAATAATATAGCACT 3639
Qy 2524 CAAGTTGAGCTGAAGAGGACACACTTCTGCGCGCCAGAAACAAAGAACTAGCTATTGCA 2583
Db 3640 AAAGTAGAGACAAAGGAACCTACGCTCTCTGCTGCGCCAGAAACCAACCATTTGCGATAGCT 3699
Qy 2584 AGGGCTCTTCTCCAAACCCCAAAATTTATTTGTTGATGAGGCCACTTTCAGCGCTCGAT 2643
Db 3700 CGTGGCTTGTAGACAGCCCTCATATTTGCTTTTGGATGAGCCACGTCAGCTCTGGAT 3759
Qy 2644 AATGAGCTGAGAGGTTGTTGATGCGCTTCTGATTAAGCCAGGACGGGAGAGCATGC 2703
Db 3760 ACAGAAAGTGAAGAGTGTCTCAAGAGCCCTGACAAAGCCAGAGAGGCGCACCTGC 3819
Qy 2704 CTAGTGGTCACTCACAGCTCTCTGCAATTCAGAACGAGATTTGATGTTGTTCTGCAC 2763
Db 3820 AATGAGTGTCTACCGCTGTCCACCATCCGATTCGAGCTTAATGTTGTTGTTTTCAG 3879
Qy 2764 AATGAGAAAGATAAGGACCAAGGAACCTATCAAGAGCTCTTCAAGAAATCGAGACATAT 2823
Db 3880 AATGCGAGATCAAGGAGCATGGACGATCAGCAGCTGCTGGCACAGAAAGGATCTAT 3939
Qy 2824 TTTAAGTTAGTGAATGCACAGTCAG 2848
Db 3940 TTTTCAATGGTCAGTGTCCAGGCTG 3964

RESULT 9

US-09-306-417-2

Sequence 2, Application US/09306417

Patent No., 6548301

GENERAL INFORMATION:

APPLICANT: Heinrich-Pette-Institut

TITLE OF INVENTION: Retroviral Gene Transfer Vectors

FILE REFERENCE: P50491

CURRENT APPLICATION NUMBER: US/09/306,417

CURRENT FILING DATE: 1999-05-06

EARLIER APPLICATION NUMBER: DE 198 22 115

EARLIER FILING DATE: 1998-05-08

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 2

LENGTH: 8630

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: proviral

OTHER INFORMATION: plasmid DNA

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(8630)

OTHER INFORMATION: retroviral expression vector SPbeta91msAI

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(160)

OTHER INFORMATION: plasmid backbone (pUC)

FEATURE:

NAME/KEY: misc feature

LOCATION: (161)..(677)

OTHER INFORMATION: 5'-LTR

FEATURE:

NAME/KEY: 5'UTR

LOCATION: (532)..(1219)

FEATURE:

NAME/KEY: mat peptide

LOCATION: (1220)..(5062)

OTHER INFORMATION: msAI mdr1 cDNA

FEATURE:

NAME/KEY: misc feature

LOCATION: (5215)..(5774)

OTHER INFORMATION: 3'-LTR

FEATURE:

NAME/KEY: misc feature

LOCATION: (5775)..(8630)

OTHER INFORMATION: plasmid backbone (pUC)

US-09-306-417-2

Query Match 36.0%; Score 1028.6; DB 4; Length 8630;

Best Local Similarity 62.2%; Pred. No. 1e-287;

Matches 1694; Conservative 0; Mismatches 989; Indels 42; Gaps 3;

Qy 166 ATTATTGATAAGAAACCCAGTATAGATAACTTTTCCACAGCTGGATATAAACCCTGAATCC 225
Db 2321 ATATTTGATTAATAGCCAAAGTATTGACAGCTATTGCAAGAGTGGGCACAAACAGATAAT 2380
Qy 226 ATAGAAGGAACCTGTGGAATTTAAAAATGTTTCTTCAATATTCATCAAGACCAATCTATC 285
Db 2381 ATTAAGGGAAATTTGGAAATTCAGAAATGTTCACTTCAGTTACCCATCTCGAAAAAGATT 2440
Qy 286 AGATTTCTGAAGTCTGATCTCAGATTAAGTCTGAGAGACAGCTCCCTTGTGCTGGT 345
Db 2441 AGATCTTGAAGGCTCTGAACCTGAGGTGAGAGTGGCGACAGCGTGGCCCTGTTTGA 2500
Qy 346 CTCAATGGCAGTGGGAAGAGTAGCGTGTGCTGAGAGTCTGCGAGAGTTATATGATCCGGAT 405
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Qy 406 GATGGCTTTTATCATGTGTGATGAGATGACATCAGAGCTTTAAATGTGGCGATTATCGA 465
Db 2561 GAGGGATGGTCACTGTTGATGACAGGATATTAGAACCAATTAATGTAAGTTTCTACGG 2620
Qy 466 GACCATATTGGAGTGTGTAGTCAAGAGCTGTTTGTTCGGACCAACCAATCAAGTAAACAAT 525
Db 2621 GAAATCATTTGGTGTGTGAGTCAGGAACCTGTATTGTTTGGCCACCACGATAGCTGAAAAC 2680
Qy 526 ATCAAGTATGGACAGATGATGTGATGATGAAGATGAGAGATGAGAGACAGCAGAGGAGCA 585
Db 2681 ATTGGCTATGGCGCTGAAAATGTCAACATGGATGAGATTGAGAAAGCTGTCAAGGAAGCC 2740
Qy 586 AATGCGTATGATTTATCATGGAGTTTCTTAATAATTTAATACATTTGTTAGGGGAAAAA 645
Db 2741 AATGCTATGACTTTATCATGAACCTGCTCATTAATTTGACACCTGTTGAGAGAGAGA 2800
Qy 646 GGAGCTCAATAGAGTGGAGGCGAGAAACAGAGAGATCGCAATTCGTCGTCCTTAGTTCGA 705
Db 2801 GGGGCCAGTTGAGTGGTGGCAGAGCAGAGAGATCGCCATTTGCACTGCTGCTGCTGCTG 2860
Qy 706 AACCCCAAGATTCTGATTTTATGATGAGGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
Db 2861 AACCCCAAGATCTCTGCTGATGAGGCGACGTCAGCTTGGACACAGAGAGGAGCA 2920
Qy 766 GCTGTTCAAGCTGCACTGGAGAGGCGAGCAAGGTTCGAGCTACAAATTCGTTGTTAGCACAC 825
Db 2921 GTGGTTCAAGTGGCTCTGATTAAGGCGCAAGAAAGGTTCGAGACCACTTTGTGATAGCTCAT 2980
Qy 826 CGACTTTTCTACTATTGGAAGTGCAGATTTTGTGTCACCTTAAGGATGGAATGCTGCTGGCG 885
Db 2981 CGTTTGTCTACAGTTCGTAAATGCTGACGTCATCGCTGGTTTCGATGATGAGTCAATGTG 3040
Qy 886 GAGAAAGGAGCACATGCTGAACTTAATGGCAAAACGAGGCTCTATATTATTCACTTGTGATG 945
Db 3041 GAGAAAGGAAATCATGATGAATCACTGAAGAGAAAGGCAATTTACTTCAAACTTGTGACACA 3100

QY 946 TCACAGGATATTAAAGAGCTGATGAACAGATGAGTCAATGACATATTCTA----- 997
DB 3101 ATGCAGACAGCAGGAATGAGTTGATAGAAAATGCAGCTGATGATCCAAAGTGAA 3160
QY 998 -----CTGAAGAAAGACCAATCTCACTTCTCTGCACTCTGTGAAGAGATCA---- 1045
DB 3161 ATTGATGCTTGGAAATGCTTCAAAATGATCAAGATCCAGTCTAAATAAGAAAAAGATCA 3220
QY 1046 -----AGTCAGACTTCATTTGACAAGGCTGAGGAATCCACCATCT 1086
DB 3221 ACTGATGAGGTGCTCGTGGATCACAAGCCACAGACGAAAGCTTAGTACCAAGAGGCT 3280
QY 1087 AAAGAGATAGTCTTCTGAAGTCTCTCTATTAAATAATTTAAAGTTAAACAGCCTGAA 1146
DB 3281 CTGGATGAAGATATACCTCCAGTTTCTTTTGGAGGATTAAGCTAAATTTAACTGAA 3340
QY 1147 TGGCCCTTTCTGGTCTGCGGACATTTGGCTTCTGTTCTAAATGGAAGTCTTCACTCAGTA 1206
DB 3341 TGGCCCTTATTGTTGGTGTGATTTTGGCCATTTAATTAAGAGGCTTGCACACCGCA 3400
QY 1207 TTTTCCATCATCTTTCCAAAAATTAATACCATGTTTGGAAATTAATATAAAACCAATTA 1266
DB 3401 TTGCAATTAATAATTTCAAAGATTAAGGGGTTTTTACAAGAAATTCATGATCTGAAACA 3460
QY 1267 AAG---CATGACAGAAATTTATTCAGATGATATTCGTCAATTTTGGGTGTTATTTGCTTT 1323
DB 3461 AAACGACAGAAATAGTAACTTTTCTCACTAATTTTCTAGCCCTTGGAAATTAATTTCTTT 3520
QY 1324 GTCAAGTATTTCATGACAGGATTAATTTACGGCAGACGAGGGAATTTTAAAGATGACA 1383
DB 3521 ATTACATTTTCTTCAAAGTTTCAATTTGGCAAGCTTGGAGATCTCTACCAAGCGG 3580
QY 1384 TTAAAGACATTTGGCTTTCAAAGCCATGTTATATCAGGATATTCGTCAATTTTGGGTGTTATTTGCTTT 1443
DB 3581 CTCCGATACATGTTTCCGATCCATGCTCAGACAGGATGAGTTGGTTTGTATGACCTT 3640
QY 1444 GAAACAGCAGCAGGAGCTTGACAACAATATAGCCATAGATATAGCAAAATTCAGCA 1503
DB 3641 AAAACACCACTGAGCATTTGATCCAGCTCGCCCAATGATGCTCTCAAGTTAAAGG 3700
QY 1504 GCAACAGGTTCCAGGATGCGCTTTAAACAATAATGCAAAATGCAACTAACATGGGACTTTCAAGTT 1563
DB 3701 GCTATAGTTCCAGGCTTGGTGAATTAATCCAGAAATATAGCAAAATTCGGGACAGGAATA 3760
QY 1564 ATCAATTTCTTTATATATGATGAGGAGATGACATTTCTGATTTCTGAGTATTTGCTCAGTA 1623
DB 3761 ATTATATCTTCTATCTATGTTGGCACTTAACACTGTTACTCTTACCAATTTGACCCATC 3820
QY 1624 CTTGCGCTGACAGGAATGATTTGAAACCGCAGCAATGACTGGATTTGCCAACAAAGATAAG 1683
DB 3821 ATTGCAATAGCAGGACTTCTTGAATGAAATGTTGTTCTGGACAAGCACTGAAAGATAAG 3880
QY 1684 CAAGAATCTTAAGCATCTGGAAGATAGCAACTGAAGCTTTGGAGAAATATACGTACTATA 1743
DB 3881 AAAGAATAGAAAGTCTGGAAGATCGCTACTGAAGCAATAGAAAACTTCCGAACCGTT 3940
QY 1744 GTGCTATTAAAGGAAAGACCTTCGAGCAATGATGAGAGATGCTTCAGACTCAA 1803
DB 3941 GTTCTTTGACTCAGGAGCAAGGTTTGAACATATGATGCTGAGAGTTGCAAGGTACCA 4000
QY 1804 CACAGAAATACCTCGAAGAACACACAGATTAATTTGGAAGCTGTTTATGCATTCAGCCATGCC 1863
DB 4001 TACAGAAATCTTTTGAAGAAACACACATCTTTTGAATTAATTTTCTTCAACCCAGGCA 4060
QY 1864 TTTTATATATTTTCCCTATGACAGGCTTCCGATTTTGGAGCTTATTTAATTCAGCTGGA 1923
DB 4061 ATGATGATTTTCTTATGCTGATGTTTCCCGTTTGGAGCTTACTTGGTGGCACAATAA 4120
QY 1924 CGAATGACCCAGAGGCGATGTTTCATAGTTTCTTACTGCAATTTGCATATGAGCTATGGCC 1983
DB 4121 CTGATGAGCTTTGAGGATGTTCTGTTAGTATTTTCAAGTGTGTTCTTTGGGCGCATGGCC 4180
QY 1984 ATCGAAAAACGCTGTTTGGCTCTCTGATATTTCCAAAGCCAAATCGGGGCGCTGCGCAT 2043

DB 4181 GTGGGCGAAGTCAGTTTCATTTGCTCTGACTATGCCAAAGCCAAAATATATCAGACGCCAC 4240
QY 2044 CTGTTTGCCTTTGTTGSAAGAAAGAACCAATATATAGACAGCCGAGTCAGAAAGGGAAGAG 2103
DB 4241 ATCATCATGATCATTTGAAAAAACCCTTTTGTATGACAGTACAGCACCGGAGCCCTAATG 4300
QY 2104 CCAGACATGTTGAAGGCAATTTAGAGTTTTCAGAGTTTTCAGAGTCTCTTTCTTCTATCTGCTGC 2163
DB 4301 CGAACACATTTGGAAGGAAATGTCACATTTGGTGAATGTTGATTCACTATCTCCACCCGA 4360
QY 2164 COAGATGTTTTCATCTCTCGTGGCTTTATCCCTCAGTATTTAGCGGAGGAAAGACAGTAGGA 2223
DB 4361 CCGACATCTCCAGTCTTTCAGGCACTGAGCCCTGAGAGTGAAGAGGCGCAGACGCTGGCT 4420
QY 2224 TTTTGGGGAGCAGCGCTGTGGGAAAGACACTTCTGTTTCAACTTCTGACAGAGCTTTAT 2283
DB 4421 CTGTTGGGACAGTGGCTGTGGGAAGACACAGTGTGTCAGCTCTCTGGAGCGGTTCTAC 4480
QY 2284 GACCCCTGCAAGGACAAAGTCTGTTGATGGTGGATGCANAAAGAAATGGAATGTACAG 2343
DB 4481 GACCCCTTGGCAGGAAAGTCTGCTGATGGCAAGAAATAAAGCGACTGAATGTTTCAG 4540
QY 2344 TGGCTCCGTTCCCAATAGCAATCGTTCTCAAGAGCTGTGCTCTTCAACTGACGACTT 2403
DB 4541 TGGCTCCAGCACACCTGGGCACTCGTCCAGGAGCCCATCTCTGTTGACTGACGACTT 4600
QY 2404 GCTGAGAACATCGCTATGTTGTCACAAAGCCCTGTGGTGCCTATAGATGAGATCAAGAA 2463
DB 4601 GCTGAGACATTTGCTATGGAGACACACAGCCGGTGTGTGCACAGAAAGAGATCGTAGG 4660
QY 2464 GCCGCAATGACGCAAAATATCATTTCTTTTATTTGAGGTCTCCCTGAGAAATACACACA 2523
DB 4661 GCAGCAAGGAGGCGCAACATATGCTCTTCTATGAGTCACTGCTTAATAATATAGCACT 4720
QY 2524 CAAGTTGCACTGAAAGGAGCAGCTTTCTGCGGCGCAGAAACAAAGACTAGCTATTGCA 2583
DB 4721 AAAGTAGAGACAAAGGAACTCAGCTCTCTGTTGGCAGAAACACGCAATTTGCCATAGCT 4780
QY 2584 AGGGCTCTTTCCAAAAACCCAAATTTTATTTTGTGATGAGGCGCACTTACGCCCTCGAT 2643
DB 4781 CTTGCCCTTTGTAGACAGCTCATATTTTGTCTTTTGTGATGAAGCCACGCTGCTGAT 4840
QY 2644 AATGACAGTGAAGAGTGGTTTCCAGCATCTTGTAAAGCCAGGACCGGAGGACATGC 2703
DB 4841 ACAGAAAGTGAAGAGTTGTCCAGAAAGCTTGGCAAGCCAGAGAGGCGGACCTGC 4900
QY 2704 CTAGTGTCTACTCAGAGCTCTCTGCAATTCAGAACCGCAGATTTGATAGTGTCTGCAC 2763
DB 4901 ATTGGAATGCTCAGCGCTGTCCACCATCCAGATGACAGACTTAATAGTGTGTTTCAG 4960
QY 2764 AATGGAAGATGAAGGAGGAGGACTCATCAGAGCTCTGAGAAATCGAGACATATAT 2823
DB 4961 AATGCGAGATCAAGGAGATGGCAGCATCAGCAGCTGCTGGCACAGAAAGGCACTAT 5020
QY 2824 TTTAAGTTAGTGAATGCACAGTCAG 2848
DB 5021 TTTTCAATGTCAGTCTCCAGGCTG 5045

RESULT 10
US-09-023-655-1168
; Sequence 1168, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE	1620	GGGGCCAGCTGAGTGGGGCAGAGACAGAGATCGCCATTGCGAGTCCCTGGTTCCG	1679	
CITY: PALO ALTO	QY	706	AAACCCAAAGATTCTGATTTTAGATGAGGCTACGTCTGCCCTCGGATTTCAGAAAGCAAGTCA	765
STATE: CALIFORNIA	Db	1680	AAACCCAAAGATCCTTCTGCTGGATGAGGCCACAGTCAAGTTCAGACACAGAAAGTGAAGCT	1739
COUNTRY: USA	QY	766	GCTGTTCAAGCTGCACTGGAGAGGCGAGCAAGGTCGGACTACAACTCGTGTGTAGCACAC	825
ZIP: 94304	Db	1740	GAGGTACAGGCGAGCTCTGGATAGGCCAGAGAGGCCGAGACCCATTGTTGTATAGCACAC	1799
COMPUTER READABLE FORM:	QY	826	CGACTTCTTACTATTTCGAAGTGCAGATTGATTGTGACCCCTAAAGGATGGAATGCTGGCG	885
MEDIUM TYPE: Floppy disk	Db	1800	CGACTGTCTACGCTCCGAAATGCAGATGTCATCGCTGGGTTTGGAGGATGGAGTAATGTTG	1859
COMPUTER: IBM PC compatible	QY	886	GAGAAAGGAGCACATGCTGAACATAATGCGCAAAACGAGGCTCTATATTATTCACTTGTGAT-	944
OPERATING SYSTEM: PC-DOS/MS-DOS	Db	1860	GAGCAAGGAAGCCACAGCGAACTGATGAAGAGGAGGGGTGATCTTCAAACCTTGTCAAC	1919
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2	QY	945	-----GTCACAGGATATTAAAAAGCTGATGAACAGAGT	978
APPLICATION NUMBER: US/09/023,655	Db	1920	ATGCAGACATCAGGAAGCCAGATCCAGTCAGAGAAATTTGAACATAATGATGAAGAGGCT	1979
FILING DATE: HEREWITH	QY	979	GAGTCAATGACATATTCTACTGAAAGAAAGACCAACTCCTCTCTGCACTCTGTGAAG	1038
CLASSIFICATION:	Db	1980	GCCACTAGAAATGGCCCCAAATGGCTGGAAATCTCGCCTATTTAGGCATTCTTACTCAGAAA	2039
PRIOR APPLICATION DATA:	QY	1039	AGCATCAAGTCAGACTTCATTGACAAAGC-----TGAGGAATCCACCAATCTAAAGAG	1092
APPLICATION NUMBER:	Db	2040	AACCTTAAAAATTCACAAATGTGTGAGAGAGCCTTGATGGAAACCGGATGCACTTGAA	2099
FILING DATE:	QY	1093	ATAAGTCTTCTGAAAGTCTCTCTATTAAAAATTTTAAAGTTTAAACAGGCTGAATGGCCT	1152
ATTORNEY/AGENT INFORMATION:	Db	2100	GCAAAATGTGCCACACAGTGTCTTCTGAAGTCTCTGAACTGAATAAAACAGAAATGGCC	2159
NAME: Zeller, Karen J.	QY	1153	TTTGTGGTCTGGGGACATGSCCTTCTGTCTTCTAATGGAACCTGTTTCATCCAGTATTTTCC	1212
REGISTRATION NUMBER: 37,071	Db	2160	TACTTTGCTGGGAAAGATGTCGCCATTTGCCAATGGGGGCTTCAGCCGCAATTTTCA	2219
REFERENCE/DOCKET NUMBER: PA-0001 US	QY	1213	ATCATCTTTGCAAAAATTTATAACCATGTTTGGAAATAATGATAAAACCACTTAAGCAT	1272
TELECOMMUNICATION INFORMATION:	Db	2220	GTCAATATCTCAGAGATCATAGCGATTTTGGACAGCGCATGATGSCAGTGAAGCAGCAG	2279
TELEPHONE: (650) 855-0555	QY	1273	GATGCAAGAAATTTATCCATGATATTCGTCAATTTGGGTGTTATTGCTTTGTCAGTTAT	1332
TELEFAX: (650) 845-4166	Db	2280	AAGTCAACATATCTCTTTGATTTTCTATTTCTGGGAATATTTCTTTTTTACTTTC	2339
INFORMATION FOR SEQ ID NO: 1168:	QY	1333	TTCATGCGAGGATTTTACGGCAGAGCAGGGGAAATTTTAAACGATCAGATTAAAGAC	1392
SEQUENCE CHARACTERISTICS:	Db	2340	TTCTTTCAGGGTTTCACTTTGGGAAAGCTGGCGAGATCCTCACCAAGAGCTGCGGTCA	2399
LENGTH: 3924 base pairs	QY	1393	TTGGCTTTCBAGCCATGTTATATCAGGATATTGCTGGTTTGTGTAAGAAAGGAAACAGC	1452
TYPE: nucleic acid	Db	2400	ATGGCTTTTAAAGCAATGCTAAGACAGGACATGAGCTGGTTTGTGACCATAAACAGT	2459
STRANDEDNESS: single	QY	1453	ACAGGAGGCTTGACAAACAAATATTAGCCATAGATATAGCACAAATTTCAAGGAGCAACAGT	1512
TOPOLOGY: linear	Db	2460	ACTGGTGCACTTTCTACAGACTTGCACAGATGCTGCCAAGTCCCAAGGAGCCACAGCA	2519
IMMEDIATE SOURCE:	QY	1513	TCAGAGATTGGGCTTTTAAACAAATGCAACTAACATGAGGACTTTCAGTTATCATTTCC	1572
LIBRARY: GENBANK	Db	2520	ACCAGGTTGGCTTTTAAATTTGCAAGATATAGTAACTTGGAACTGGTATTATCATATCA	2579
CLONE: g187501	QY	1573	TTTATATATGATGGGAGATGCAATTTCTCTGATTTCTGAGTATTGCTCCAGTACTTCCCGT	1632
US-09-023-655-1168	Db	2580	TTTATCTACGGTTGCGCAGTTAAACCTTATTTGCTATTAGCAGTTGTTTCCAATTTGCTGTG	2639
Query Match 36.08; Score 1027.2; DB 4; Length 3924;	QY	1633	ACAGGAATGATTGAAACCGCAGCAATGACTGGAATTTGTCACAAAGATTAAGCAAGACTT	1692
Best Local Similarity 61.9; Pred. No. 1.7e-287;	Db	2640	TCAGGAATTTGTTGAATGAAATTTGTTGGCTGGAAATGTCAAAAGAGATATAAAGACTG	2699
Matches 1682; Conservative 0; Mismatches 1003; Indels 33; Gaps 2;	QY	1693	AAGCAATGCTGGAAGATAGCAACTGCAAGCTTTGGAGAATATACGTACTATATAGTTCATTA	1752

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1168:

SEQUENCE CHARACTERISTICS:

LENGTH: 3924 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: g187501

US-09-023-655-1168

Query Match 36.08; Score 1027.2; DB 4; Length 3924;

Best Local Similarity 61.9; Pred. No. 1.7e-287;

Matches 1682; Conservative 0; Mismatches 1003; Indels 33; Gaps 2;

QY 166 ATTATTGATAAGAAACCCAGATAGATAAATCTTTTCCAGCTGGATATAAATCACTGAATCC 225

Db 1140 ATTATTGATAAATCTTAAATTTGACAGTTTTTCAGAGAGAGACACAAACAGACAGC 1199

QY 226 ATAGAAGGAACTGTGGAAATTTTAAAAATGTTTCTTTCAAATTCATTCATCAAGCAATCTATC 285

Db 1200 ATCAAAGGGAATTTGAGTTCAATGATGTTCACTTTTCTTACCTTCTCGAGCTAACGTC 1259

QY 286 AAGATCTGAAAGGCTCGAATCTCAGAAATTAAGTCTGGAGAGACAGTCGCTTGGTGGT 345

Db 1260 AAGATCTTGAAGGGCTCAACTGAGGTGAGAGTGGGCGAGCGTGGCCCTGGTTGA 1319

QY 346 CTCATAGGCACTGGGAAGAGTAGTCGGTAGTCAGCTTCTCGAGAGTTATATGATCCGGAT 405

Db 1320 AGTAGTGGCTGTGGGAAGAGCAACCGTCCAGCTGATACAGAGGCTCTATGACCCCTGAT 1379

QY 406 GATGCTTTATCATGCTGGATGAGATGACATCAGAGCTTTAAATGTGGGCAATATCGA 465

Db 1380 GAGGCAACATTAACATTTGATGGCAGGATATTAGCACTTTAATGTAAACTATCTGAG 1439

QY 466 GACCAATATGGAGTGGTTAGTCAAGAGCCTGTTTGTGTGGGACCAACATCAGTAACAT 525

Db 1440 GAAATCATGTGTGTGGTGTGAGTCAGAGCGGTGCTGTTTTCACCACAATTTGCTGAAAT 1499

QY 526 ATCAAGTATGCAAGATGATGTGACTGATCAAGAGATGGAGAGCAGCAAGGGAAGCA 585

Db 1500 ATTTCATTGCGCTGTGGAAATGTAAACCATGATGAGATAAGAAAGCTGTCAAAGGCC 1559

QY 586 AATGCGTATGATTTTATCATGAGGTTTCTTAATTAATTTAATATCATTTGGTAGGGGAAAA 645

Db 1560 AACGCGCTATGATTTTATCATGAAATTTACACAGAAATTTGCACCCCTGGTTGGAGAGA 1619

QY 646 GGAGCTCAATGAGTGGAGGCGAGAAACAGAGGATCGCAATTTGCTGCTTGTAGTTGGA 705

us-09-873-409-10.rni

Db 2700 GAAGCTGCTGGAAGATTGCAACAGAGGCAATAGAAAATATTAGGACAGTTGTGCTTTG 2759
Qy 1753 ACAGGGAAAAAGCCTTCGAGCAATGATGAAGAGATGCTCAGACTCAACACAGAAAT 1812
Db 2760 ACCAGGAAGAAAAATTGAATCAATGATGTTGAAATTTGATGAGCTTTACAGGAAT 2819
Qy 1813 ACCTGAAAGAACACAGATTTATTGGAAGCTGTTATGCAATTCAGCCATGCCCTTATATAT 1872
Db 2820 TCTGTGCAGAGGACACACATCTATGAAATTTACTTTTAGTATCTCACAGCAATTTATGAT 2879
Qy 1873 TTGCTCTATGACAGAGGTTTCGATTTGAGCCCTATTATTAATCAAGCTGGAGCAATGACC 1932
Db 2880 TTTTCTATGCGCGTTTGTTCGATTTGATGTTGCAATCTCATTTGTGAATGGACATATGCGC 2939
Qy 1933 CCAGAGGCAATGTTTCATAGTTTTTACTGCAATTCGATATGAGCTATGCGCATCGGAAAA 1992
Db 2940 TTTGAGAGATGTTATCTGTTGTTTCTGCAATTTGTTATTTGTCAGTGTCTGAGCAAT 2999
Qy 1993 ACCTCGTTTGTGCTCTGCAATTCCTAAAGCCAAATTCGAGGCTCGCATCTGTTTGGC 2052
Db 3000 GCCAGTTCTATTTGCTCCAGACTATGCTAAAGCTGAAGCTGCTGCAAGCCACTATTATG 3059
Qy 2053 TTGTTGAAAGAAACCAATATAGACAGCGGAGTCAAGAGGGAAGGAAAGCCAGACACA 2112
Db 3060 CTGTTTGAAGACAACTCTGATTGACAGTACAGTGAAGAGGGGCTGAAGCTGTATAA 3119
Qy 2113 TGTGAAGGAATTTAGAGTTTTCAGAGAGTCTCTTCTTCTATCCATGTCGCCAGATGTT 2172
Db 3120 TTTGAAGGAATATAATTTAATGAATGCTGTTCAACTATCCACCCGAGCAAGGTTG 3179
Qy 2173 TTTATCTCTGCTGCTTATCCCTCAGTATGAGGAGGAAAGACAGTATGTTTGGG 2232
Db 3180 CCAGTCTCTCAGGGCTGAGCCTGGAGGTGAAGAAAGGCGAGACTAGCCCTGTTGGG 3239
Qy 2233 AGCAGCGGCTGCGGAAAGCACTCTGTTCACTTCTGAGAGACTTTTATGACCCCGT 2292
Db 3240 AGCAGTGGCTGTGGAAGAGCAAGTGTCCAGCTCTTGAGCGGTTCTAAGACCCCTT 3299
Qy 2293 CAAGGCAAGTGTCTGTTGATGTTGGAATGCAAAAGAAATGAATGTAAGTGGCTCGT 2352
Db 3300 GCGGGGACAGTGTCTCGATGCTCAAGAGCAAGAAAGAACTCAATGTCCAGTGGCTCAG 3359
Qy 2353 TCCCAATATAGCAATCTCTCTCAAGAGCTGTGCTCTCACTGAGAGCTGCTGAGAC 2412
Db 3360 GCTCACTCGAATCTGTCTCAGGAGCTTCTTAATTTGACTGAGCAATTTCCGAGAT 3419
Qy 2413 ATGCTCTATGTCAGAACCGCTGTGGTGTCCATTTAGATGAGATCAAGAAAGCCGAAT 2472
Db 3420 ATTGCTTATGAGAACACAGCGGTTGTTATCACAGATGAATTTGAGTGCAGCAAA 3479
Qy 2473 GCGAGCAATATCCATCTTTTATTGAGGTCTCCCTGAGAAATACACACAAAGTTGGA 2532
Db 3480 GCTGCCAACATACATCTTTCTACGAGAGCTTACCCCAAAATATGAAGAGAGTGGGA 3539
Qy 2533 CTGAAGAGGACACNGCTTTCTGCGGCCAGAAACAAAGACTAGCTATTGCAAGGCTCTT 2592
Db 3540 GATAAGGGGACTCAGCTCTCAGAGGTCAAAACAGAGGTTGCTATTGCCCGAGCCCTC 3599
Qy 2593 CTCCAAAACCCAAAATTTTATTGTTGATGAGGCCACTTCAGCCCTCGATATGACAGT 2652
Db 3600 ATCAGACAACCTCAATCTCTCTGTTGATGAGCTTACATCAGCTCTGATCTGCAAGT 3659
Qy 2653 GAGAGGCTGTTTCCAGATGCTTGAATAAGCCAGGACGAGGAGGACATGCTAGTGTGTC 2712
Db 3660 GAAAGGTTGTCCAGAGAGCCCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2719
Qy 2713 ACTCAGAGCTCTCTGCAATTCAGAACGAGATTTGATAGTGTCTGCAATGGAAG 2772
Db 3720 GCTCAGCGCTGTCCACCATCCAGATGAGACTTAATAGTGTGTTTTCAGAAATGGAGA 3779
Qy 2773 ATAAAGGACAGGAATCTCATAGAGCTCTCAGAGAAATCAGACATATTTTAACTTA 2832
Db 3780 GTCAAGGAGATGGCAAGCATCAGAGCTGCTGGCAAGAAAGGCAATCTATTTTCAATG 3839

Qy 2833 GTGAATGCACAGTCAAGT 2850
Db 3840 GTCAGTGTCCAGGCTGG 3857
RESULT 11
US-09-762-195-2
; Sequence 2, Application US/09762195
; Patent No. 6677319
; GENERAL INFORMATION:
; APPLICANT: Stremler, Wolfgang
; TITLE OF INVENTION: Phosphatidylcholine as Medication with
; FILE OF INVENTION: Protective Effect on Large Intestinal Mucosa
; FILE REFERENCE: 34691/208520
; CURRENT APPLICATION NUMBER: US/09/762,195
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: PCT/EP99/02426
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 198 35 526 2 DE
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 198 57 570.8 DE
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3924
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-762-195-2

Query Match 36.0%; Score 1027.2; DB 4; Length 3924;
Best Local Similarity 61.9%; Pred. No. 1.7e-287;
Matches 1682; Conservative 0; Mismatches 1003; Indels 33; Gaps 2;

Qy 166 ATTATGATAGAAACCCAGTATAGATAACTTTCCAGCTGGATATAAACCCTGAATCC 225
Db 1140 ATTATGATATAATATCTTAAATTTGACAGTTTTCAGAGAGGAGACAAACAGACAGC 1199
Qy 226 ATAGAAGGAATGTGGAATTTAAATAATGTTCTTTCAATTTCCATCAAGACCATCTATC 285
Db 1209 ATCAAAGGAATTTGGAGTTCAATGATGTTTACATTTTCTTACCTTTCTCGAGCTAACGTC 1259
Qy 286 AGATTTCTGAAAGTCTGAATCTGAAATTAAGTCTGGAGAGACAGTGCCTTGGTGGT 345
Db 1260 AAGATCTTTGAAGGGCTCAACCTGAAGGTGAGAGTGGGAGAGCGTGGCTGGTTGGA 1319
Qy 346 CTCATGTCAGTGGAGAGTACGGTAGTCTCAGCTTCTGAGAGGTTTATATGATCCGGAT 405
Db 1320 AGTAGTGTCTGTGGAAGGACACACGCTCAGCTGATACAGAGGCTCTATGACCTGAT 1379
Qy 406 GATGCTTTTATCATGTTGGATGAGATGATCATCATGAGCTTTAAATGTGCGGCAATTATCGA 465
Db 1380 GAGGCAATTAACATTTGATGGGAGGATATTAGGAACCTTTAATGTAAACTATCTGAGG 1439
Qy 466 GACCATATTGGAGTGGTTAGTCAAGAGGCTGTTTGTTCGGGACCACCATCAGTAACAT 525
Db 1440 GAATCATGTTGTGTTGAGTCAAGGCGGCTGCTGTTTTTCCACCAATTTGCTGAAT 1499
Qy 526 ATCAAGTATGAGAGAGATGATGTGACTGATGAAGAGATGGAAGAGAGAGAGAGAGAG 585
Db 1500 ATTTGTTATGCGGTGAATATGTAACCATGATGATGATGAAGAGAGCTGTCAAAGAGGCC 1559
Qy 586 AATGCTGATGATTTTATCATGAGTTCCTTAATAATTTATATGATGCTAGGAGGAAAA 645
Db 1560 AACGCTATGATGTTTATCATGAATTTACCAAGAAATTTGACACCTCGTGGAGAGAGA 1619
Qy 646 GGAGCTCAAATGAGTGGAGGCGGAGAAAACAGAGGATCGCAATTTGCTGCTGCTTATGTCGA 705
Db 1620 GGGGCCAGCTGAGTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1679
Qy 706 AACCCCAAGATTTGATTTTATGATGAGCTAGCTGCTGCTGCTGATTCAGAAAGCAATGCA 765

Db 1680 AACCCCAAGATCTCTTCTGCTGGATGAGGCCACGTGACGATTTGGACACAGAAAGTGAAGCT 1739
Qy 766 GCTGTTCAAGCTGCACTGGAGAGCGCAGCAAGCTCGGACTACAATCTGTTGGTAGCACAC 825
Db 1740 GAGGTACAGGCAGCTCTGATATAGGCCAGAGAGCGCGGACCACCATTTGTATAGCACAC 1799
Qy 826 CGACTTCTACTATTGCGAAGTGCAGATTTGATGAGCCCTTAAGAGATGGAATGCTGCGC 885
Db 1800 CGACTGCTACGGTCCGAAATGCGAATGTCATGCTGCTGGTTTGGAGATGGAATTTGTG 1859
Qy 886 GAGAAAGGAGCACATGCTGAATTAATGCAAAAGAGCTCTATATTACTTCTGTCAT- 944
Db 1860 GAGCAGAGAGCCACAGCACTGATGAGAGAGAGAGGGGTGACTTCAAACTTGTCTAC 1919
Qy 945 -----GTCCAGGATATTAAAAAGCTGATGAGACAGATG 978
Db 1920 ATGCAGACATCAGGAAGCCAGATCCAGTCAAGAGATTTGAACTAAATGATGAAAGGCT 1979
Qy 979 GAGTCAATGACATATTCTACTGAAAGAGAGCAACCTCACTCTCTGCACTCTGCTGAAG 1038
Db 1980 GCCACTAGATGGCCCAATGGCTGGAAATCTCGCTATTAGGCAATTTCTACTCAGNAA 2039
Qy 1039 AGCATCAAGTCAGACTTCAATGCAAGGC-----TGAGGAATCCACCCTAATCTAAAGAG 1092
Db 2040 AACCTTAAAAATTCNMAATGTGTGAGAGAGCCTTGATGTGGAACCGATGGACTTGAA 2099
Qy 1093 ATAGTCTTCTGCTGAGTCTCTCTATTAAATTTTAAAGTTAAACRAGCCTGATGGCCT 1152
Db 2100 GCAATGTGCCACAGGTCTCTTCTGAGGTCTCTGAAACTGTAATAAAACAGATGGCCC 2159
Qy 1153 TTTGTGTTCTGGGGACATTTGGCTTCTGTTCTAAATGGAATGTTCTCATCCAGTATTTTC 1212
Db 2160 TACTTTGCTGGGAAACAGTATGTGCCATTTGCCAATGGGGCTTCAGCCGGCATTTTCA 2219
Qy 1213 ATCATCTTTGAAAAATTATACCATGTTTGGAAATTAATGATAAACCAATTAAAGCAT 1272
Db 2220 GTCATATTCTCAGAGATCATAGCAATTTTGGACGCGCATGATGCAATGAAAGCAG 2279
Qy 1273 GATGCAAGAAATTTATTCATCATATTGCTCATTTTGGTGTATTGCTTTTGTGAGTTAT 1332
Db 2280 AAGTGCAACATTTCTCTTGTATTCTATTCTGGAATTTTCTTTTACTTTC 2339
Qy 1333 TTCAATGCGGAATTTATTACGGCAGAGCAGGGGAAATTTTACGATGAGATTAAGACAC 1392
Db 2340 TTCTTCAGGGTTTTCAGCTTTGGGAAAGCTGGGAGATCTCCACCAAGACTGGGTCA 2399
Qy 1393 TTGGCTTCAAGGCATGTTATATCAGATATTCCTGCTTTGATGAAAGGAAACAGC 1452
Db 2400 ATGGCTTTAAGCAATGCTAAGACAGACATGAGCTGGTTTGTATGACCATAAACAGT 2459
Qy 1453 ACAGAGCTTGAACAAATATTAGCCATGATATAGCAAAATTTCAAGAGCAACAGGT 1512
Db 2460 ACTGTCACCTTTCTACAAGACTTGCACAGATGCTGCCAAAGTCCAAAGGAGCCACAGGA 2519
Qy 1513 TCCAGGATTTGGCTTTAAACAAATGCAACTAACATGGGACTTTTCAGTTTATCATTTCC 1572
Db 2520 ACCAGTTGGCTTTAATTGACAGATATAGCTTAACTTGGACTGGTATTATCATATCA 2579
Qy 1573 TTTATATATGATGGGAGATGACATTTCTGATCTGATATTGCTCCAGTACTTGGCGTG 1632
Db 2580 TTTATCTACGGTTGGCAGTTAAACCTATTGCTATTAGCAGTTGTTCCAAATTTATGCTGTG 2639
Qy 1633 ACAGGATGTTGAAACCGCAGCAATGACTGATTTGCCAACAGATAGCAGACTT 1692
Db 2640 TCAGGAATTTTGAATGAAATTTGTTGGCTGGAATTTCCAAAGAGATAAAGAAAGACTG 2699
Qy 1693 AAGCATGCTGGAAGATAGCAACTGAAGCTTTGGAGAAATATAGTACTATAGTGTCAATTA 1752
Db 2700 GAAGCTGCTGGAAGATTGCAACAGAGCAATAGAAATATTAGGACAGTTGTGCTTTG 2759
Qy 1753 ACAAGGAAAAAGCCTTCAGCAATATGATGAGAGATGCTTCAGACTCAACAGAAAT 1812
Db 2760 ACCAGGAAAAAGAAATTTGAATCAATGATGTTGAAAAAATTTGATGAGACCTTACAGAAAT 2819

Qy 1813 ACCTCGAAGAAAGCACAGATTTATTTGGAAGCTGTTATGCAATTCAGCCATGCCTTTATATAT 1872
Db 2820 TCTGTGCAAGAGGCACACATCTATGGAATTTACTTTTAGTATCTCAACAAGATTTATGTAT 2879
Qy 1873 TTTGCTTATGACAGCAGCGTTTCGATTTTGGAGCTTATTTAATTTCAAGCTGGAAGAAAGAC 1932
Db 2880 TTTTCTTATGCGGTTTGTGTTTTCGATTTGTCATATCTCATTTGTAATGGAATATGCGC 2939
Qy 1933 CCAGAGGCGATGTTTCATAGTTTTTAACTGCAATTTGCAATATGAGAGCTATGAGCAATCGGAAA 1992
Db 2940 TTCAGAGATGTTATTTCTGGTGTCTTCTGCAATTTGTTGTTGTCAGTGGCTCTAGGACAT 2999
Qy 1993 AGCTCGTTTGGCTCTCTGAATATTTCCAAAGCCAAATCGGGGCTCGGCACTGTTTGGC 2052
Db 3000 GCCAGTTCTATTTGCTTCAGACTATGCTAAAGCTAAGCTGCTCTGCAAGCCACATTTATTCATG 3059
Qy 2053 TTGTTGAAAAAGAAACCAATATAGACAGCCGAGTCAAGAGAGGAAAAAGCCAGACACA 2112
Db 3060 CTGTTTGAAGACACACTCTGATTTGACAGTACAGTGAAGAGGGCTGAAGCTGTATAA 3119
Qy 2113 TGTGAAGGAATTTAGAGTTTCGAGAAAGTCTCTTCTTCTATCCATGTCGCCAGATGTT 2172
Db 3120 TTTGAAGGAATATAACATTTAATGAAGTCGTGTTCAACTATCCACCCGAGCAACGTTG 3179
Qy 2173 TTCATCTCCGTGGCTTATCCCTCAGTATTGAGCGAGAAAGACAGTACATTTGTGGG 2232
Db 3180 CCAGTCTTTCAGGGCTGAGCTTGAGGTGAAGAGAGCCAGACACTAGCCCTGTTGGC 3239
Qy 2233 AGCAGCGGCTGTGGAAAAACATTTCTGTTCAACTTTCTCAGAGACTTTTATCAACCCCTG 2292
Db 3240 AGCAGTGGCTGTGGGAAGACAGCGTGTCTCAGCTCTCTGGAGCGGTTCTACGACCCCTG 3299
Qy 2293 CAAGGACAGTCTGTTGATGTTGGATGCAAAAGAAATGCAATGTACAGTGGCTCCCT 2352
Db 3300 GCGGGACAGTGTCTCTCGATGTTCAAGAGCAAAAGAACTCAATGTCAGTGGCTCAGA 3359
Qy 2353 TCCAAAATAGCAATCGTTCTCAAGAGCCTGTGCTCTTCAACTGCAAGCAATTTCTGAGAAC 2412
Db 3360 GCTCAACTCGGAATCGTGTCTCAGGAGCTATCTTATTTGACTGTCAGCAATTTGCCAGAAT 3419
Qy 2413 ATGCTTATGTTGACAAACAGCCGTGTGTCCTATTTAGATGATCAAGAGAGCCCAAT 2472
Db 3420 ATTGCTTATGAGAGCAACAGCCGGTGTGATCACAGGATGAAATTTGAGTGCAGCCAAA 3479
Qy 2473 GCAGCAAAATATCCATTTCTTTTATGGAAGCTCTCCCTGAGAAATACAAACAAGTTGGA 2532
Db 3480 GCTGCCAACATATCTTTTCAATCGAGAGCTTACCCCAAAATATGAAACAAGAGTGGGA 3539
Qy 2533 CTGAAAGGAGCAAGCTTTCTGCGGCCGAGAAACAAAGACTAGCTATTTCAGAGGCTCTT 2592
Db 3540 GATAAGGGGACTCAGCTCTCAGGGGTCAAAAACAGAGGATTTGCTATTGCCCAGCCCTC 3599
Qy 2593 CTCCAAAAACCCAAAAATTTTATTTGTTGATGAGGCCACTTTCAGCCCTCGATTAATGACAGT 2652
Db 3600 ATCAGACAACTCAATCTCTCTGTTGATGAGCTACATCAGCTCTGATACTGAAAGT 3659
Qy 2653 GAGAGGTTGTTTCAGATGCTCTTATTAAGCCAGAGCGGAGAGCAATGCTCTAGTGGTC 2712
Db 3660 GAAAAAGTTTGTCCAAAGAGCCCTTGGACAAAGCCAGAGAGGCCGACCTCTGCTATTTGAT 3719
Qy 2713 ACTCAGAGCTCTCTGCAATTCAGAAAGCAGATTTGATGTTGTTCTGCAATGGAAG 2772
Db 3720 GCTACCGCTGTCTCAACCATCCAGATGAGACTTAATAGTGTGTTTTCAGATGGAGA 3779
Qy 2773 ATAAAGGAACAAAGGAATCATCAAGCTCTCTGAGAAATTCGAGACATATATTTTAAGTTA 2832
Db 3780 GTCAAGGAGACTGGCAACGATCAGCAGCTGCTGGCACAGAAAGGCTATCTATTTTCAATG 3839
Qy 2833 GTGAATGCACTCAGTG 2850
Db 3840 GTCAGTGTCCAGGCTGGG 3857

2561 GAGGGGATGGTTCAGGTGTGATGACAGGAGATTTAGGACCATAAATGTATGAGTCTTCTACGG 2562

466 GACCATATTGGAGTGGTTAGTCAAGAGCCTGTTTGTTCGGGACCAACATCAGTAAACAAT 535

2621 GAAATCAATTGGTGTGGTGAAGTCAAGAAACCTGTATTGTTTGGCCACACGATAGCTGAAAC 2680

526 ATCAAGTATGACAGAGATGATGTCATGATGAAGAGATGGAGAGACGACGCAAGGGAAGCA 585

2681 ATTGCTATGGCCGTGAATGTCAACATGATGAGATTGAGAAAGCTGTCAAGGAAGCC 2740

586 AATCGTATGATTTTATCATGAGGTTTCCCTAATAAATTAATAATCATTTGGTAGGGGAAAAA 645

2741 AATGCTATGACTTTATCATGAAATGCGCTCATAAATTTGACACCCCTGGTTGGAGAGAGA 2800

646 CGAGCTCAATAGAGTGGAGGCGCAGAAACAGAGGATCGCAATTCGTCGTGCTTAGTTCGA 705

2801 GGGGCCAGTTGAGTGTGGCAGACGACAGAGATCGCATTTGCATGTGCCCTGGTTCGC 2860

706 AACCCCAAGATTCTGATTTTATGATGAGGCTACGTTCTGCCCTGGATTCAGAAAGCAAGTCA 765

2861 AACCCCAAGATCCCTGCTGGATGAGGCCACGTCAGCGCTTTGGACACAGAAAGCGAAGCA 2920

766 GCTGTTCAAGCTGACATCGAGAGGCGAGCAAGAGTCCGACTCAACTCGTGGTAGACAC 825

2921 GTGGTTCAAGTGGCTCTGGATAGGCCCAAGAAAGTCCGACCAACATTTGTATGATCTCAT 2980

826 CGACTTTCTACTATTGAAAGTCGACGATTTGATTTGTGACCCCTAAAGGATGAAATGCTGGCG 885

2981 CGTTGTCTACAGTTCTGATGTCAGCTCATCGCTGGTTTCGATGATGAGTCAATGTG 3040

886 GAGAAAGGACATGCTGGAATTAATGGCAAAACGAGTCTATATTATTCACTTGTGATG 945

3041 GAGAAAGGAATCATGATGAATCTATGAAAGAAAGAGGCAATTTACTTCAAACTGTGACA 3100

946 TCACAGGATATTAAGAAAGCTGATGAACAGATGGAGTCAATGACATATTTCTA----- 997

3101 ATGCAGACAGCAGGAAATGAAGTTGAAATTTAGAAAATGCAGCTGATGAATCCAAAAGTGA 3160

998 -----CTGAAAGAAAGACCAACTCACTCTCTGCACCTGTGGAAGAGCATCA--- 1045

3161 ATTGAGCCTTGGAAATGCTTCAATGATTTCAAGTCCAGTCTAATAAGAAAGATCA 3220

1046 -----AGTCAGACTTTCATGCAAGGCTGAGGAATCCACCCCAATCT 1086

3221 ACTGATGAGAGTGTCCGTGGATCACAAAGCCCAAGACAGAAAGCTTAGTACCAAGAGGCT 3280

1087 AAGAGATAGTCTTCTGAGTCTCTCTATTAATAATTTTAAAGTTAAACAGGCTGAA 1146

3281 CTGAGTGAAGATATACCTCAAGTTCCCTTTGGAGGATATGAGCTTAAATTTAACTGAA 3340

1147 TGGCCTTTTGTGTTCTGGGACATTTGGCTCTGTTCTAAATGAACTGTCTATCCAGTA 1206

3341 TGGCCTTATTGTTGTGTGTGATTTTGTGCCAATATAAATGAGGCCCTGCAACCAAGCA 3400

1207 TTTTGCATCATCTTCCAAAATATATACATGTTTGGAAATATGATTAACACCAATTA 1266

3401 TTTGCAATAATAATTTCAAAGATATAGGGGTTTTTCAAGAAATGATGATCTGTAACA 3460

1267 AAG---CATGATGAGAAATTTATTCATATGATATTCGTCATTTTGGGTGTTATTTCCTTT 1323

3461 AAAAGCAGAAATAGTAAGTTTTCATATTGTTCTAGCCCTTGGAAATTAATTTCTTTT 3520

1324 GTCTGATTATTTCAATGACGGATTAATTTACGGCAGACAGGGGAAATTTTAAAGATGAG 1383

3521 ATTAATCAATTTTCTCAAGGTTTTCATTTGGCAAGCTGGAGAGATCTCTCAACAAGGG 3580

1384 TTATAGACATTTGGCTTTCAAAGCCATGTTATATCAGGATATGTCCTTGTTTGAATGAAAG 1443

3581 CTCGGATACATGTTTTCGATCCATGCTCAGACAGGATGTGTAGTTGTTTGTATGACCT 3640

1444 GAAACAGACACAGAGGCTTGAACAACAATAATTAGCCATGATATAGCAAAATTCAGGA 1503

3641 AAAAACACCACTGGACATTTGATACACAGGCTCGCCATGATGCTGCTCAAGTAAAGG 3700

Qy	1504	GCAACAGGTTCCAGGATTGGCGTCTTTAAACAACAATGCAACTAACATGGGACTTTTCAGTT	1563
Db	3701	GCTATAGGTTCCAGGCTTGCCTGTAAATTACCCAGAATATAGCAAAATCTTGGGACAGGAATA	3760
Qy	1564	ATCATTTCCCTTTATATATGGATGGCAGATGACATTTCTCGATTCGTGAGTATTCGTCACAGTA	1623
Db	3761	ATTATATCCCTTCATCTATGGTTGSCAACTAACACTGTCTACTCTTAGCAATTGTACCCATC	3820
Qy	1624	CTTGCCGTGACAGGAATGATTTGAAACCGCAGAGTAAGACTGGAATTTGGCCACAAGATATAAG	1683
Db	3821	ATTCCAAATAGCAGGAGTTGTTGAAATGAAAATGTTGTCTGGACAAGCACCTGAAAGATAAG	3880
Qy	1684	CAAGAACTTAAAGCATGCTGGAAAGATAGCAACTGAAGCTTTTGGHGAATATACGTACTATA	1743
Db	3881	AAAGAACTAGAGGTGCTGGGAGATCGCTACTGAAGCAATAGAAACTTCCGAAACCGTT	3940
Qy	1744	GTGTCAATTACAGGGGAAAAAGCCTTCGAGCAATGATTAAGAGATGCTTCAGACTCAA	1803
Db	3941	GTATCTTTGACTCAGGAGCAGAAAGTTTGAACATATGATGTCTCAGAGTTTGCAGGTACCA	4000
Qy	1804	CACAGAAATACCTCGAAAGAACACACATTAATTGGGAAGCTGTTATGCATTCAGCCATGCC	1863
Db	4001	TACAGAAACTCTTTGAGAAAGCACACATCTTTGGAAATTACATTTTCCTTCACCCAGGCA	4060
Qy	1864	TTTATATATTTGCTATGACAGCAGGGTTTCGATTTGGAGCCTATTTPAATTCAGACTGGA	1923
Db	4061	ATGATGTATTTTCTATGCTGSGATGTTCCGGTTTGGAGCCTACTTTGGTGGCACATAA	4120
Qy	1924	CGAATGACCCAGAGGGCAGTTCATATGTTTTTACTGCAATTCGATATGAGTATGAGTATGGCC	1983
Db	4121	CTCATAGACTTTTGAAGATGTTCTCTTAGTATTTTCAGCTGTGTCTTTGTTGTCATATGGCC	4180
Qy	1984	ATCGGAAAAACCGCTCGTTTTGGCTCTCTGAAATATTCGAAAGCCAAATCGGGGGCTGGGCAT	2043
Db	4181	GTGGGCGAAGTCAGTTCAATTTGCTCTCTGACTATGCCAAAGCCAAAATATCAGCAGCCAC	4240
Qy	2044	CTGTTTGGCCTTGTGGAAAGAAACCAATATAGACAGCCGCACTCAAGAGGGAAGAAAG	2103
Db	4241	ATCATATCATATGAAATGTGAAAAACCCCTTTGATTGACAGCTACAGCAGGAAGGCCCTAATG	4300
Qy	2104	CCAGACACATGTGAAGGGAATTTAGAGTTTCGAGAGTCTCTTTCTTCTATCCATCTGCG	2163
Db	4301	CCGAAACATTTGGAAGGAAATGTCCATTTGGTGAAGTTGATTTCAACTATCCACCCGA	4360
Qy	2164	CCAGATGTTTTTCATCCTCCGTGGCTTATCCGTACGATTTGAGCAGGAAAGACAGTAGCA	2223
Db	4361	CCGACATATCCAGTCTTTCAGGGACTCAGCCTCGAGGTGAAGGCCACAGACGCTGGCT	4420
Qy	2224	TTTGTGGGAGCAGCGCTGTGGGAAAAGACATCTCTCTTCAAATCTCTGACAGACTTTTAT	2283
Db	4421	CTGTGTGGCAGCATGTGCTGTGGGAAAGACACAGTGTGTCCAGTCTCTGGAGCGGTTCTAC	4480
Qy	2284	GACCCCGTGCAGACAAAGTCTGTTTATGTTGTGTGATGCAAGAAATTTGAATGTACAG	2343
Db	4481	GACCCCTTGGCAGGAAAGTGTCTCTTTGATTTGGCAAGAAATTAAGCGACTGAAATGTTCAG	4540
Qy	2344	TGGCTCCGTTTCCCAAAATAGCAATCGTTTCTTCAAGAGCCTGTGCTCTTCAACTTCGACATT	2403
Db	4541	TGGCTCCGAGCACACCTTGGGCAATCGTGTCCAGAGGCCATCTCTGTTGACTTCGACATT	4600
Qy	2404	GCTGAGAACATTCGCTATGTGTGAACAAGCCGTGTGTGCAATTAGATAGATATCAAGAA	2463
Db	4601	GCTGAGAACATTTGCTATTTGAGACAACAGCGGGTGTGTCAAGGAAGATTCGTGAGG	4660
Qy	2464	GCCGCAATGACGAAATATCCATCTCTTTTATTTGAAGTCTCTCCTGAGAAATACAAACA	2523
Db	4661	GCAGCAAGGAGGCCAACATACATATGCTTTCATGAGTCACTGCTCTAATAATATAGCACT	4720
Qy	2524	CAAGTTGACTGAAAGGAGCACAGCTTTCTGGCGGCCAGAAAAACAAGACTAGTCTATTGCA	2583
Db	4721	AAAGTAGGAGACAAGGAACTCAGCTCTCTGTTGGCCAGAAAACAACCAATGCACTAGCT	4780

2584 AGGCTCTTCTCCAAAACCAAAATTTATTTGATGAGGCCACTTCAGCCCTCGAT 2684
4781 CGTCCCTTGTATAGACAGCTCATATTTTCTTTTGGATGAAGCCACGTCAGCTCTCGAT 4840
2644 AATGACAGTGAAGAGGTGGTTTCAGCATGCCCTTGTATAAAGCCAGGACCGGAAGGACATGC 2703
4841 ACAGTAGTGAAGAGGTGTCCAGAGAGCCCTGGAAGAGCCAGAGAGGCCGACCTGC 4900
2704 CTAGTGCTACTCACAGGCTCTCTGCAAAATTCAGAAAGCAGATTGATAGTGGTTCTGCAC 2763
4901 ATTGTGATTGCTCACCCGCTGTCCACCATTCCAGAAATGCAGACTTAATAGTGGTTTCAG 4960
2764 AATCGAAGATGAAGGAACAGAGGAACTCATCAGAGCTCTCTGAGAAATCGAGACATATAT 2823
4961 AATGECAGAGTCAAGAGAGCTGGCCAGCATCGCAGCTGCTGSCACAGAAAGGATCTAT 5020
2824 TTTAAGTTAGTGAATGCACAGTTCAG 2848
5021 TTTTCAATGGTTCAGTGTCCAGGCTG 5045

RESULT 13
US-08-583-276-18
; Sequence 18, Application US/08583276
; Patent No. 5837536
; GENERAL INFORMATION:
; APPLICANT: McDonagh, Kevin T.
; APPLICANT: Niemhuis, Arthur
; APPLICANT: Tolstoshev, Paul
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
; TITLE OF INVENTION: SELECTION OF CELLS TRANSFECTED WITH SUCH GENES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DNA V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,276
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/332,444
; FILING DATE: 31-OCT-1994
; APPLICATION NUMBER: 07/887,712
; FILING DATE: 22-MAY-1992
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4669 bases
; TYPE: nucleic acid
; STRANDEDNESS: singular
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: Genomic DNA
US-08-583-276-18

Db 3746 TGGCTCCGAGCACACCTGGGCACTGTCCTCCAGGAGCCCATCTGTTTGAATGACGCAATT 3805
Qy 2404 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 2463
Db 3806 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 3865
Qy 2464 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 2523
Db 3866 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 3925
Qy 2524 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 2583
Db 3926 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 3985
Qy 2584 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 2643
Db 3986 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 4045
Qy 2644 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 2703
Db 4046 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 4105
Qy 2704 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 2763
Db 4106 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 4165
Qy 2764 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 2823
Db 4166 GCTGAGAACATCGCTATGTTGGAACAAGCGCGTGTGTGCTGATGAGATCAAGAA 4225
Qy 2824 TTTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2848
Db 4226 TTTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4250

RESULT 14

US-08-752-447-1
; Sequence 1, Application US/08752447
; Patent No. 594088
; GENERAL INFORMATION:
; APPLICANT: Mechnether, Eugene
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Methods and Reagents for Preparing and
; TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehrner Hulbert & Berghoff Ltd.
; STREET: 300 South Wacker Drive, Seventh Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,447
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 594088nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 95,1121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-9808
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4669 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
US-08-752-447-1
Query Match 35.8%; Score 1022.2; DB 2; Length 4669;
Best Local Similarity 62.0%; Pred. No. 5.2e-286;
Matches 1690; Conservative 0; Mismatches 993; Indels 42; Gaps 3;
Qy 166 ATATTGATGAAGAACCCAGTATAGATAACTTTTCCACAGCTGGATATTAACCTGATTC 225
Db 1526 ATAATTGATGAAGAACCCAGTATAGATAACTTTTCCACAGCTGGATATTAACCTGATTC 1585
Qy 226 ATAGAAGGAACCTGTGGAATTTTAAATGTTCTTTCAATATTCATCAAGACCATCTATC 285
Db 1586 ATAGAAGGAACCTGTGGAATTTTAAATGTTCTTTCAATATTCATCAAGACCATCTATC 1645
Qy 286 AAGATTCTGAAGGCTCTGAATCTCAGATTAAGTCTGAGAGACAGTCTGCTTGGTTCGGT 345
Db 1646 AAGATTCTGAAGGCTCTGAATCTCAGATTAAGTCTGAGAGACAGTCTGCTTGGTTCGGT 1705
Qy 346 CTCATATGGCAGTGGGAGAGTACGCTAGTCCAGCTTCTGACAGAGTTATATGATCCGGAT 405
Db 1706 AAGATTCTGAAGGCTCTGAATCTCAGATTAAGTCTGAGAGACAGTCTGCTTGGTTCGGT 1765
Qy 406 GATGGCTTTATCATGTTGGATGAGATGACATCAGAGCTTTTAAATGTCGGCATTTATCGA 465
Db 1766 GATGGCTTTATCATGTTGGATGAGATGACATCAGAGCTTTTAAATGTCGGCATTTATCGA 1825
Qy 466 GACCATATTTGGAGTGTAGTCAAGAGCCTGTTTCTGCGGACCAACCATCAGTACCAAT 525
Db 1826 GATGGCTTTATCATGTTGGATGAGATGACATCAGAGCTTTTAAATGTCGGCATTTATCGA 1885
Qy 526 ATCAAGTATGAGACAGATGATGCTGATGATGATGATGATGATGATGATGATGATGATG 585
Db 1886 ATCAAGTATGAGACAGATGATGCTGATGATGATGATGATGATGATGATGATGATGATG 1945
Qy 586 AATGCTATGATTTTATCATGTTGGATGAGATGACATCAGAGCTTTTAAATGTCGGCATTT 645
Db 1946 AATGCTATGAGACAGATGATGCTGATGATGATGATGATGATGATGATGATGATGATG 2005
Qy 646 GAGAGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 705
Db 2006 GAGAGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2065
Qy 706 AATGCTATGATTTTATCATGTTGGATGAGATGACATCAGAGCTTTTAAATGTCGGCATTT 765
Db 2066 AATGCTATGAGACAGATGATGCTGATGATGATGATGATGATGATGATGATGATGATG 2125
Qy 766 GCTGTTCAAGCTGACATGAGAGAGGCGAGCAAGAGTCCGACATCAATCGTGGTAGCACAC 825
Db 2126 GCTGTTCAAGCTGACATGAGAGAGGCGAGCAAGAGTCCGACATCAATCGTGGTAGCAC 2185
Qy 826 CGACTTTTCTACTATTCGAAAGTGCAGATTTGATGTCGACCCCTAAAGGATGGAATGCTGG 885
Db 2186 CGACTTTTCTACTATTCGAAAGTGCAGATTTGATGTCGACCCCTAAAGGATGGAATGCTGG 2245
Qy 886 GAGAAAGGAGCACATCTGAACCTAAATGCGCAACAGAGGCTATATTTATTCACCTTGTGATG 945
Db 2246 GAGAAAGGAGCACATCTGAACCTAAATGCGCAACAGAGGCTATATTTATTCACCTTGTGATG 2305
Qy 946 TCACAGGATATTTAAAGAGCTGATGAACAGATGAGTCAATGACATATTTCTA----- 997
Db 2306 TCACAGGATATTTAAAGAGCTGATGAACAGATGAGTCAATGACATATTTCTA----- 2365

COMPUTER READABLE FORM:			
MEDIUM TYPE:	Floppy disk		
COMPUTER:	IBM PC compatible		
OPERATING SYSTEM:	PC-DOS/MS-DOS		
SOFTWARE:	Patentin Release #1.0, Version #1.30		
CURRENT APPLICATION DATA:			
APPLICATION NUMBER:	US/09/316.167		
FILING DATE:			
CLASSIFICATION:			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER:	08/752.447		
FILING DATE:	15-NOV-1996		
ATTORNEY/AGENT INFORMATION:			
NAME:	No. 636537nan, Kevin E		
REGISTRATION NUMBER:	35,303		
REFERENCE/DOCKET NUMBER:	95,1121		
TELECOMMUNICATION INFORMATION:			
TELEPHONE:	312-913-0001		
TELEFAX:	312-913-9808		
INFORMATION FOR SEQ ID NO: 1:			
SEQUENCE CHARACTERISTICS:			
LENGTH:	4669 base pairs		
TYPE:	nucleic acid		
STRANDEDNESS:	single		
TOPOLOGY:	linear		
MOLECULE TYPE:	CDNA		
FEATURE:			
NAME/KEY:	5'UTR		
LOCATION:	1..424		
FEATURE:			
NAME/KEY:	CDS		
LOCATION:	425..4264		
FEATURE:			
NAME/KEY:	3'UTR		
LOCATION:	4265..4669		
US-09-316-167-1			
Query Match			35.8%; Score 1022.2; DB 4; Length 4669;
Best Local Similarity			62.0%; Pred. No. 5.2e-286;
Matches 1690; Conservative 0; Mismatches 993; Indels 42; Gaps 3;			
Qy	166	ATTATTGATAAGAAACCCAGTATAGATAAATTTTCCACAGCTGGATATAAACCTGAATCC	225
Db	1526	ATAATTGATATAAGCCAAAGTATTGACAGCTATTGGAAGTGGCGCAACACCAAGATAAT	1595
Qy	226	ATAGAGGAAGCTGGGAATTTAAATATGTTTCTTCAATTTATCCATCAGACCATCTATC	285
Db	1586	ATTAAGGGAAATTTGGAATTCAGAAATGTTCACTTCAGTTACCCATCTCGAAAGAGTT	1645
Qy	286	AAAGTTCTGAAGGCTCGAATCTCAGAATTAAGTCTGGAGAGACAGTCCGCTTGGTCGGT	345
Db	1646	AGATCTTGAAGGCTTGAACCTGAAGTGGAGAGTGGCGACAGCGTGCCCTTGGTTGA	1705
Qy	346	CTCAATGGCAGTGGGAAGTACGGTAGTCCAGCTTCTGCGAGAGTATATATGATCCGGAT	405
Db	1706	AAACAGTGGCTGGGAAGAGCACAACAGTCCAGCTGATGCGAGAGCTTATGACCCACA	1765
Qy	406	GATGCTTTATCATGCTGGATGAGATGACATCAGAGCTTTAAATGTGCGGCATTATCGA	465
Db	1766	GAGGGATGGTGGTTGATGGACAGAGTATAGACCAATATATGTAAGTTTCTACGG	1825
Qy	466	GACCAATTGGAGTGGTTAGTCAAGAGCTGTTTGTGTTGGGACCAACATCAGTAACAAT	525
Db	1826	GAATCAATTGGTGGTGGTGGAGAACTGTATGTTTGGCCACCAACAGTATGTAAGAAC	1885
Qy	526	ATCAAGTATGCGAGATGATGTGACTGATGAGAGATGGAGAGCAGCAGCAGGAGCA	585
Db	1886	ATTGCTATGGCCGGTGAATGTGACCATGATGATGATGAGATGATGAGAGCTGTCAAGAGCC	1945
Qy	586	AATGGCTATGATTTTATCATGAGTGTTCCTATATAAATTTAATATGTTGGTGGGAAAAA	645
Db	1946	ATGCTATGACTTTTATCATGAAGAACTGCTCATAAATTTGACACCCCTGGTTGGAGAGA	2005

Qy	646	GGAGCTCAATGAGTGGAGGGCAGAAAACAGAGGATCGCAATTCGTGCTGTAGTTGCA	705
Db	2006	GGGGCCAGTTGAGTGGTGGGAGAGCAGAGGATCGCAATTCGCACTGCTGCTGCTGCG	2065
Qy	706	AACCCCAAGATTCTGATTTTATGATGAGGCTACGTCTGCTGCTGATTCAGAAACAGTCA	765
Db	2066	AACCCCAAGATCTCTGCTGCTGATGAGGCTACGTCTGCTGCTGATTCAGAAACAGTCA	2125
Qy	766	GCTGTTCAAGCTGCTGCTGAGAGGGGAGCAAGAGTGGCAACTCAATCTGTTGATGACAC	825
Db	2126	GTGTTTCAAGTGGCTCTGATAGGGCCAGAAAGGTCGACCCCACTTGTGATAGTCAAT	2185
Qy	826	CGACTTTCTACTATTCGAAAGTGCAGATTTGATGTCACCTTAAGGATGGAATGCTGGCG	885
Db	2186	CGTTTGTCTACAGTTCGTAATGCTGACGTCATCGCTGGTTTGGATGATGAGTCAATGTG	2245
Qy	886	GAGAAAGGAGCAGCATCTGCAACTTAATGGCAAAACGAGGTCATATTAATTCACATTGATG	945
Db	2246	GAGAAAGGAAATCATGATGAACTCATGAAAGAGAAAGGATTTTACTTCAACTTGTGACA	2305
Qy	946	TCACAGGATATTAAAAAGCTGATGAACAGATGGAGTCAATGACATATTCTTA	997
Db	2306	ATGCAGACAGCAGGAAATGAAGTTGAATTAGAAAATGCAGCTGATGAATCCAAAGTAA	2365
Qy	998	-----CTGAAAGAAAGACCAACTCACTCTCTGCACTCTGTCAGAGAGATCA---	1045
Db	2366	ATTGATGCCCTTGGAAAATGCTTCAAAATGATTCAGATGCCAGTCTAATAAGAAAAGATCA	2425
Qy	1046	-----AGTCAGACTTCAATTCAGCAAGGCTGAGGAATCCACCCATCT	1086
Db	2426	ACTGCTAGGAGTGTCTGATGATCACAAGCCCAACACAGAAAGCTTAGTACCAAGAGGCT	2485
Qy	1087	AAAGATTAAGTCTTCTGAGTCTCTCTATTAAATAATTTAAAGTTAAACAGCTGAA	1146
Db	2486	CTGGATGAAAGTATATACCTCCAGTTCTTTTGGAGGATTTAGAAAGCTAAATTTAACTGAA	2545
Qy	1147	TGCTCTTTTGTGTTTCTGGGCAATTTGCTCTTCTTCTTAAATGGAACTGTTCATCCAGTA	1206
Db	2546	TGCTCTTTTGTGTTTCTGGGCAATTTGCTCTTCTTCTTAAATGGAACTGTTCATCCAGTA	2605
Qy	1207	TTTTCCATCACTTTTGAAATAATTAACCACTGTTTGGAAATAATGATTAACCACTTA	1266
Db	2606	TTTGCATAATATTTTCAAAGATTTAGGGGTTTTCACAGAAATGATGATCTCTGAAACA	2665
Qy	1267	AAG---CATGATGACAGAAATTTATTCATCATGATTTCTGCTTCTGCTGTTTATTTGCTTT	1323
Db	2666	AAAGCAGAAATGATTAATTTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTT	2725
Qy	1324	GTCAATTTTCTGAGGATTTTTCAGCAGAGAGGGGAAATTTTAAACGATGAGA	1383
Db	2726	ATTACATTTTCTGAGGTTTTCATTTGCAAGCTGAGAGATCTCTCAGCAGCGG	2785
Qy	1384	TTAAGACACTTGGCTTCAAGCCATTTATATCAGATATTGCTGTTTGTGATGAAG	1443
Db	2786	CTCGATACATGTTTTCGATCCATGCTCAGCAGAGTGTGAGTTGTTTCTGATCCCT	2845
Qy	1444	GAAAAACAGCAGAGGCTTGAACAATAATTAGCCATAGATATAGCAAAATTCAGGA	1503
Db	2846	AAAAACACCACTGAGCATTTGACTACAGGCTGCCAATGATGCTGCTCAAGTTAAAGGG	2905
Qy	1504	GCACAGTTCAGGATTTGCGCTTTAAACACAAATGCAACTTAACATGCGACTTTCAGTT	1563
Db	2906	GCTATAGTTTCCAGGCTGCTGTAATTTACCCAGATATAGCAAAATTTGGACAGGATA	2965
Qy	1564	ATCATTTCTTTTATATGATGGAGATGACATTCCTGATTTCTGAGTATTGCTCCAGTA	1623
Db	2966	ATTATATCTTCTATCTATGTTGCAACTTAACACTGTTACTCTTAGCAATTTGATCCCATC	3025
Qy	1624	CTTGGCTGACAGGATGATGAAACCGGCGCAATGATGATGATTTGCCCAAGATAG	1683
Db	3026	ATTGCAATAGCAGGATTTGTTGAATGAAATGTTTGTGTCGCAAGCACTGAAAGATAAG	3085
Qy	1684	CAAGAACTTAAGCATGCTGGAAGATAGCAACTGAAAGCTTTGGAGATATATACGTACTATA	1743

Qy 2824 TTTRAAGTTAGTGAATGACAGTCAG 2848
 Db 4226 TTTTCAATGGTCAGTGTCCAGGCTG 4250

Search completed: June 25, 2004, 03:53:26
 Job time : 241 secs

Db 3086 AAAGAACTAGAGGTGCTGGAGATCGCTACTGAAGCAATAGAAACTTCGAACGGTT 3145
 Qy 1744 GUGTCATTAAACAGGGAAGCCCTCGAGCAATGTTGAAGAGATGCTTCAGACTCAA 1803
 Db 3146 GTTCTCTTGACTCAGGAGCAAGAGTTGAACATATGATGCTCAGAGTTTGAGGTACCA 3205
 Qy 1804 CACAGAAATACCTCGAAGAAAGCACAGATTATGGAAGCTGTTATGCAATTCAGCCATGCC 1863
 Db 3206 TACAGAACTCTTTGAGGAAGCACACATCTTTGGAAATACATTTTCTTCAACCCAGGCA 3265
 Qy 1864 TTTATATATTTGCCATGACAGAGGTTTCGATTTTGGAGCCTATTATTAATTAAGCTGGA 1923
 Db 3266 ATGATGATATTTTCTTATGCTGGATGTTCCGGTTTGGAGCCTACTTGGTGGCACATAA 3325
 Qy 1924 CGAATGACCCACAGAGGCTGTTCAATAGTTTCTTACTGCAATTCATATGAGCTATGGCC 1983
 Db 3326 CTATGAGCTTTGAGGATGTTCTGTTAGTATTTTTCAGCTGTTGCTTGGTGCATGGCC 3385
 Qy 1984 ATCGGAAAAACGCTCGTTTGGCTCCTGGAATATTCGAAAGCCAAATTCGGGGGCTGCGCAT 2043
 Db 3386 GTGGGCAAGTCAGTTTCAATTTGCTGCTGACTATGCAAGAGCCAAATATCAGCAGGCCAC 3445
 Qy 2044 CTGTTTGCCTTGTGGAAGAACCAATATAGACGCGCAGTCAAGAGGGGAAG 2103
 Db 3446 ATCATCATGATCATTTGAAAGAACCCCTTTGATTTGACAGCTACAGCAGGAGGCTTATG 3505
 Qy 2104 CCAGACACATGTGAAGGGAATTTAGAGTTTCGAGAGTCTCTTTCTTCTATCCATGTGCG 2163
 Db 3506 CCGAACACATTTGAAGGAATGTACATTTTGGTGAAGTGTATTTCAACTATCCACCCGA 3565
 Qy 2164 CCAGATGTTTTTCATCTCCGTGGCTTATCCCTGATGTTTGAAGGGAAGAGACAGTAGCA 2223
 Db 3566 CCGACATCCAGTGTCTTCAGGAGCTGAGCTGAGGTTGAAGAGGCGCCAGAGCTGGCT 3625
 Qy 2224 TTTGTGGGAGCAGCGGCTGTGGGAAAGCACTTCTTCAACTTCTGCAGAGACTTTAT 2283
 Db 3626 CTGGTGGGAGCAGTGGCTGTGGAGAGACACAGTGTCCAGCTCCTGGAGCGGTTCTAC 3685
 Qy 2284 GACCCCTGCAAGACAGAGTGTCTTTTGTGATGTTGATGCAAGAAATTAATGTTACAG 2343
 Db 3686 GACCCCTTGGCAGGGAAGTGTCTTTGATGGCAAGAAATAAAGCGACTGAATGTTTCAG 3745
 Qy 2344 TGGCTCGTTTCCAAATAGCAATCGTTTCTCAAGAGCTGTGCTTCTCACTGCGCAT 2403
 Db 3746 TGGCTCCGAGCACACCTGGGCAATCGTGTCCAGAGGCCATCTGTTTGTGCTGAGGAT 3805
 Qy 2404 GCTGAGAACATTCGCTATGTGCAACAGCGGTTGTGGCCATTAGATGAGATCAAGAA 2463
 Db 3806 GCTGAGAACATTGCTTATGAGACACAGCGGTTGTGTCAAGGAAAGAGATCGTGAGG 3865
 Qy 2464 GCCGCAATGCAAGCAATATCCATCTTTTATTGAAGTCTCCCTGAGAAATACACACA 2523
 Db 3866 GCAGAAAGGAGGCCAACATACATGCTTCAATGAGTCACTGCTTAATAATATAGACT 3925
 Qy 2524 CAAGTTGACTTGAAGAGGACACAGCTTTCTGGCGGCCAGAAACAAAGACTAGCTATTGCA 2583
 Db 3926 AAAGTAGGAGACAAAGGAACTCAGCTCTCTGTTGGCCAGAAACAAAGCATTTGCCATAGCT 3985
 Qy 2584 AGGCTCTTCTCCAAAGAACCCAAATTTTATTGTTGATGAGGCCACTTCAGCCCTCGAT 2643
 Db 3986 CGTGGCTTGTAGACAGCCTCATATTTTGTCTTTTGGATGAAGCCACGTCAGCTCTGGAT 4045
 Qy 2644 AATGACAGTGAAGAGTGTGTTTCAATGCGCCCTTGAATAAGCCAGGACGGGAAGACATGC 2703
 Db 4046 ACAGAAAGTGAAGAGTTGTTCAAGAGCCCTGACAAAGCCAGAGAGGCCGACCTGC 4105
 Qy 2704 CTAGTGTCTACACAGCTCTCTGCAATTCAGAACGAGATTTGATAGTGTCTCTCAC 2763
 Db 4106 ATTGTGATTGTCTACCGCTGTCCACCATCCAGAAATGCAGACTTAATAGTGTGTTTCAG 4165
 Qy 2764 AATGGAAGATAAGGACACAGGAACTCATCAAGGCTCCGTGGAATTCGAGACATATAT 2823


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QY 2401 ATTGCTGAGAACATGCGCTATGCTGACACAGCCGCTGTGGTGCATTTAGATGATCAAA 2460
DB 2401 ATTGCTGAGAACATGCGCTATGCTGACACAGCCGCTGTGGTGCATTTAGATGATCAAA 2460
QY 2461 GAAGCCGCAAAATGAGCAATATCCATCTCTTTTATTGAAGGCTCTCCCTCAGAAATCAAC 2520
DB 2461 GAAGCCGCAAAATGAGCAATATCCATCTCTTTTATTGAAGGCTCTCCCTCAGAAATCAAC 2520
QY 2521 ACACAGTTGGAGCTGAAGAGGACACAGCTTTCTGGCGGCAGAAAACAAGACTAGCTATT 2580
DB 2521 ACACAGTTGGAGCTGAAGAGGACACAGCTTTCTGGCGGCAGAAAACAAGACTAGCTATT 2580
QY 2581 GCAAGGGCTCTCTCCAAAACCCAAAATTTATTGTTGATGAGGCCACTTCAGGCCCTC 2640
DB 2581 GCAAGGGCTCTCTCCAAAACCCAAAATTTATTGTTGATGAGGCCACTTCAGGCCCTC 2640
QY 2641 GATAATGACAGTGAAGAGGCTGCTGAGCATGCCCTTGATAAAGCCAGGACGGGAAGACA 2700
DB 2641 GATAATGACAGTGAAGAGGCTGCTGAGCATGCCCTTGATAAAGCCAGGACGGGAAGACA 2700
QY 2701 TGCTTAGTGTCACTCACAGGCTCTCTGCAATTCAGACGCGAGTTGATGTTGTTCTG 2760
DB 2701 TGCTTAGTGTCACTCACAGGCTCTCTGCAATTCAGACGCGAGTTGATGTTGTTCTG 2760
QY 2761 CACAATGGAAGATAAAGGAACCAAGAACTCATCAAGAGCTCTCGAGAAATCGAGACATA 2820
DB 2761 CACAATGGAAGATAAAGGAACCAAGAACTCATCAAGAGCTCTCGAGAAATCGAGACATA 2820
QY 2821 TATTTTAAAGTGTGATGACAGTCAAGTGCAGTGA 2856
DB 2821 TATTTTAAAGTGTGATGACAGTCAAGTGCAGTGA 2856

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RESULT 2

US-09-873-409-12

; Sequence 12, Application US/09873409

; Patent No. US20020037522A1

; GENERAL INFORMATION:

; APPLICANT: Frank, Markus

; APPLICANT: Sayegh, Mohamed

; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein

; FILE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof

; FILE REFERENCE: 81994/268611

; CURRENT APPLICATION NUMBER: US/09/873,409

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12

; LENGTH: 3177

; TYPES: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: No. US20020037522A1

; LOCATION: (198)..(198)

; OTHER INFORMATION: n at position 198 represents any nucleotide (A, T, C or G)

US-09-873-409-12

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Query Match 94.2%; Score 2690.6; DB 9; Length 3177;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2693; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 160 TCCTCATTTATGATGAAGAACCCAGTATAGATAAGCTTTTCCACAGCTCGATATAAACCT 219
DB 481 TTCAGGTTATTGGAAGAAACCCAGTATAGATAAGCTTTTCCACAGCTCGATATAAACCT 540
QY 220 GAATCCATAGAAGAACTGTGGAATTTAAATTTCTTTCAATTTATCCATCAAGACCA 279
DB 541 GAATCCATAGAAGAACTGTGGAATTTAAATTTCTTTCAATTTATCCATCAAGACCA 600
QY 280 TCTATCAAGTTCTGAAGGCTGATCTCAGAAATTAAGTCTGGAGAGACAGTCCGCTTG 339
DB 601 TCTATCAAGTTCTGAAGGCTGATCTCAGAAATTAAGTCTGGAGAGACAGTCCGCTTG 660

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QY 340 GTCCGCTCTCAATGGCAGTGGGAGAGTAGAGTACGTTAGTCCAGCTTCTCGAGAGGTTATATGAT 399
DB 661 GTCCGCTCTCAATGGCAGTGGGAGAGTAGAGTACGTTAGTCCAGCTTCTCGAGAGGTTATATGAT 720
QY 400 CCGGATGATGGCTTTATCATGGTGGATGAAGATGACATCAGAGCTTTAAATGTGGGCAAT 459
DB 721 CCGGATGATGGCTTTATCATGGTGGATGAAGATGACATCAGAGCTTTAAATGTGGGCAAT 780
QY 460 TATCGAGACCAATATTTGGAGTGGTTAGTCAAGAGCCCTGTTTGTTCGGGACCAATCATGAT 519
DB 781 TATCGAGACCAATATTTGGAGTGGTTAGTCAAGAGCCCTGTTTGTTCGGGACCAATCATGAT 840
QY 520 AACCAATATCAAGTATGGACGAGATGATGATGATGAAGAGATGAGAGAGACGACCAAGG 579
DB 841 AACCAATATCAAGTATGGACGAGATGATGATGATGAAGAGATGAGAGAGACGACCAAGG 900
QY 580 GAAGCAAAATGCGTATGATTTTATCATGAGTTTCTTAATAAATTTAATCATGTTGTTAGGG 639
DB 901 GAAGCAAAATGCGTATGATTTTATCATGAGTTTCTTAATAAATTTAATCATGTTGTTAGGG 960
QY 640 GAAGAGAGGCTCAAAATGATGGAGGCGAGAAACAGAGGATCGCAATTTGCTCGTGCCTTA 699
DB 961 GAAGAGAGGCTCAAAATGATGGAGGCGAGAAACAGAGGATCGCAATTTGCTCGTGCCTTA 1020
QY 700 GTTCCGAACCCCAAGATTTCTGATTTTAGATGAGGCTAGCTCTGCCCTGGATTCAGAAAGC 759
DB 1021 GTTCCGAACCCCAAGATTTCTGATTTTAGATGAGGCTAGCTCTGCCCTGGATTCAGAAAGC 1080
QY 760 AAGTCAGCTGTTCAAGCTGCACTGGAGAGGCGAGCAAAAGCTGCGACCTACATTCGTTGTA 819
DB 1081 AAGTCAGCTGTTCAAGCTGCACTGGAGAGGCGAGCAAAAGCTGCGACCTACATTCGTTGTA 1140
QY 820 GCACACCCACTTTCTATTTTGAAGTGCAGATTTGATTTGTCACCTTAAAGGATGGAATG 879
DB 1141 GCACACCCACTTTCTATTTTGAAGTGCAGATTTGATTTGTCACCTTAAAGGATGGAATG 1200
QY 880 CTGGCGGAGAAAGGAGGACATGCTGAATTAATGCGCAAAACAGAGTCTATTTATTTCACTT 939
DB 1201 CTGGCGGAGAAAGGAGGACATGCTGAATTAATGCGCAAAACAGAGTCTATTTATTTCACTT 1260
QY 940 GTGATGTCACAGGATTTTAAAGAGCTGATGAACAGATGAGTCAATGACATATTTCTACT 999
DB 1261 GTGATGTCACAGGATTTTAAAGAGCTGATGAACAGATGAGTCAATGACATATTTCTACT 1320
QY 1000 GAAGAGAAAGCAAACTCTCTCTCTGCACTCTGTGGAAGAGATCAAGTCAAGCTTCAAT 1059
DB 1321 GAAGAGAAAGCAAACTCTCTCTCTGCACTCTGTGGAAGAGATCAAGTCAAGCTTCAAT 1380
QY 1060 GACAGGCTGAGGATCCACCCCACTTAAGAGATAGTCTTCTGAGTCTCTCTATTA 1119
DB 1381 GACAGGCTGAGGATCCACCCCACTTAAGAGATAGTCTTCTGAGTCTCTCTATTA 1440
QY 1120 AAAATTTTAAAGTTAAACCAAGCTGAATGGCTTTTGTGGTCTTGGGACATTTGGCTTCT 1179
DB 1441 AAAATTTTAAAGTTAAACCAAGCTGAATGGCTTTTGTGGTCTTGGGACATTTGGCTTCT 1500
QY 1180 GTTCTAAATGGAATGTTTATCCAGTATTTTCCATCATCTTTGCAAAATTAATACCATG 1239
DB 1501 GTTCTAAATGGAATGTTTATCCAGTATTTTCCATCATCTTTGCAAAATTAATACCATG 1560
QY 1240 TTTGGAAATTAATGATTAATAACCAATTAAGAGATGATGAGAAATTTATTTCCATGATATTC 1299
DB 1561 TTTGGAAATTAATGATTAATAACCAATTAAGAGATGATGAGAAATTTATTTCCATGATATTC 1620
QY 1300 GTCAATTTTGGTGTATTTGCTTTGTGATTTTATTCAGAGGATTTATTTACGGCAGA 1359
DB 1621 GTCAATTTTGGTGTATTTGCTTTGTGATTTTATTCAGAGGATTTATTTACGGCAGA 1680
QY 1360 GCAGGGGAAATTTTAAACGATGAGATTAAGACACTTTGGCTTTCAAGGATGTTATATCAG 1419
DB 1681 GCAGGGGAAATTTTAAACGATGAGATTAAGACACTTTGGCTTTCAAGGATGTTATATCAG 1740

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Qy	1420	GATATTGCTCGGTTTGGATGAAAAGGAAAAACAGCACAGGAGCGCTTGTGCAACAATATTAGCC	1479
Db	1741	GATATTGCTCGGTTTGGATGAAAAGGAAAAACAGCACAGGAGCGCTTGTGCAACAATATTAGCC	1800
Qy	1480	ATAGATATAGCACAAATTCAAGGAGCAACAGGTTCCAGGATTCGGCTCTTAAACACAAAAT	1539
Db	1801	ATAGATATAGCACAAATTCAAGGAGCAACAGGTTCCAGGATTCGGCTCTTAAACACAAAAT	1860
Qy	1540	GCAACTAAACATGGGACCTTCAGTTATCATTTCCCTTTATATATGATGGGAGATGACATTC	1599
Db	1861	GCAACTAAACATGGGACCTTCAGTTATCATTTCCCTTTATATATGATGGGAGATGACATTC	1920
Qy	1600	CTGATCTGAGTATTCGCTCCAGTACTTCGCGTGACACAGGAATGATGAAACCGCAGCAATG	1659
Db	1921	CTGATCTGAGTATTCGCTCCAGTACTTCGCGTGACACAGGAATGATGAAACCGCAGCAATG	1980
Qy	1660	ACTGGATTTGCCAACAAAGATAAGCAAGAACTTTAAGCATGCTCGAAAGATAGCAACTGAA	1719
Db	1981	ACTGGATTTGCCAACAAAGATAAGCAAGAACTTTAAGCATGCTCGAAAGATAGCAACTGAA	2040
Qy	1720	GCCTTGGAGAATATACGTACTATAGTGTCAATTAAACAGGGAANAAGCCCTCGAGCAAAATG	1779
Db	2041	GCCTTGGAGAATATACGTACTATAGTGTCAATTAAACAGGGAANAAGCCCTCGAGCAAAATG	2100
Qy	1780	TATGAAGAGATGCTTCAGAGCTCAACACAGAAAACTCCTGAAAGAAAGCACAGATTATTGGA	1839
Db	2101	TATGAAGAGATGCTTCAGAGCTCAACACAGAAAACTCCTGAAAGAAAGCACAGATTATTGGA	2160
Qy	1840	AGCTGTTATGCAATTCAGCAATGCTTTATATATATTTTGGCTATGACAGAGGTTTCGATTT	1899
Db	2161	AGCTGTTATGCAATTCAGCAATGCTTTATATATATTTTGGCTATGACAGAGGTTTCGATTT	2220
Qy	1900	GGAGCCTATTATTTCAAGCTTGGACGAATGACCCAGAGGGGCAATGTTCAATGTTTTTACT	1959
Db	2221	GGAGCCTATTATTTCAAGCTTGGACGAATGACCCAGAGGGGCAATGTTCAATGTTTTTACT	2280
Qy	1960	GCAATTGCATATGGAGCTATGGCCATCGGAAAAACGCTCGTTTTGGCTCCTGAAATATCC	2019
Db	2281	GCAATTGCATATGGAGCTATGGCCATCGGAAAAACGCTCGTTTTGGCTCCTGAAATATCC	2340
Qy	2020	AAAGCCAAATCGGGGCTGGCGATCTGTTTGGCTTGTTCGAAAGAAACCAATATAGAC	2079
Db	2341	AAAGCCAAATCGGGGCTGGCGATCTGTTTGGCTTGTTCGAAAGAAACCAATATAGAC	2400
Qy	2080	AGCGCAGTCAAGAAAGGAAAAAGCCAGACACATGTCAAGGGAATTTAGAGTTTCAGAA	2139
Db	2401	AGCGCAGTCAAGAAAGGAAAAAGCCAGACACATGTCAAGGGAATTTAGAGTTTCAGAA	2460
Qy	2140	GTCTCTTCTTCTATCCATGTCGCCAGATGTTTTGATCTCCGTGGCTTATCCCTCAGT	2199
Db	2461	GTCTCTTCTTCTATCCATGTCGCCAGATGTTTTGATCTCCGTGGCTTATCCCTCAGT	2520
Qy	2200	ATTGAGCGAGAAAGACAGTAGCATTTGTGSGGAGCAGCGCTGTGGCAAAAGCACTTCT	2259
Db	2521	ATTGAGCGAGAAAGACAGTAGCATTTGTGSGGAGCAGCGCTGTGGCAAAAGCACTTCT	2580
Qy	2260	GTTCAACTTTCGACAGACTTTATGACCCCGTGCAGGACAAGTCGTGTTGATGPGTGTG	2319
Db	2581	GTTCAACTTTCGACAGACTTTATGACCCCGTGCAGGACAAGTCGTGTTGATGPGTGTG	2640
Qy	2320	GATCCAAAGAAATTTGAATGTACGTGCTCGTTCCCAATAGCAATCGTCTCTCAAGAG	2379
Db	2641	GATCCAAAGAAATTTGAATGTACGTGCTCGTTCCCAATAGCAATCGTCTCTCAAGAG	2700
Qy	2380	CCTGTGCTCTTCAACTGCAGCAATTTGCTGAGAACATGCGCTATGGTGACACAGCGTGTG	2439
Db	2701	CCTGTGCTCTTCAACTGCAGCAATTTGCTGAGAACATGCGCTATGGTGACACAGCGTGTG	2760
Qy	2440	GTGCCATTAGATGATCAAAAGACCGCAATGACGAAATATCCATCTCTTTATTGAA	2499
Db	2761	GTGCCATTAGATGATCAAAAGACCGCAATGACGAAATATCCATCTCTTTATTGAA	2820
Qy	2500	GGTCTCCCTGAGAATAACACACAAAGTTGCATCTGAAAGAGAGCACAGCTTTCTTGGCGCG	2559

Db	2821	CCTCCTGGAAATACAAACACACAAAGTTGGATCTGAAGGACACAGCTTCTCGCGGC	2880
Qy	2560	CAGAAACAAGA CTAGCTATTGCAAGGGCTCTCTCCAAAACCCAAAATTTTATTGTTG	2619
Db	2881	CAGAAACAAGA CTAGCTATTGCAAGGGCTCTCTCCAAAACCCAAAATTTTATTGTTG	2940
Qy	2620	GATGAGGCCACTTTCAGCCCTCGATAATGACAGTGAAGAGTGTTTCAGCATGCCCTTGAT	2679
Db	2941	GATGAGGCCACTTTCAGCCCTCGATAATGACAGTGAAGAGTGTTTCAGCATGCCCTTGAT	3000
Qy	2680	AAAGCCAGGACGGGAAGGACATSCCTTAGTGGTCACCTCAGAGGCTCTCTGCAATTCAGAAC	2739
Db	3001	AAAGCCAGGACGGGAAGGACATSCCTTAGTGGTCACCTCAGAGGCTCTCTGCAATTCAGAAC	3060
Qy	2740	GCAGATTGATGTGGTCTTCGACAATGGAAGATTAAGGACACAGGACCTCATCAAGAG	2799
Db	3061	GCAGATTGATGTGGTCTTCGACAATGGAAGATTAAGGACACAGGACCTCATCAAGAG	3120
Qy	2800	CTCCTGAGAAATCGAGACATATATTTTAAGTTAGTGAATGCCAGTCAGTCAGTGA	2856
Db	3121	CTCCTGAGAAATCGAGACATATATTTTAAGTTAGTGAATGCCAGTCAGTCAGTGA	3177

RESULT 3

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RESULT 3
US-09-873-409-14
? Sequence 14 Application US/09873409
? Patent No. US20020037522A1
? GENERAL INFORMATION:
? APPLICANT: Frank, Markus
? APPLICANT: Sayegh, Mohamed
? TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
? TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
? FILE REFERENCE: 81994/268611
? CURRENT APPLICATION NUMBER: US/09/873,409
? CURRENT FILING DATE: 2001-06-05
? NUMBER OF SEQ ID NOS: 19
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 14
? LENGTH: 3621
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-873-409-14

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Query Match 94.2%; Score 2690.6; DB 9; Length 3621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2693; Conservative 0; Mismatches 4; Indels 0;

Qy	160	TCCCTCATATTGATATAGAAACCCAGCATAGATAACTTTTCCACAGCTGGATATAACCT	2119
Db	925	TTCCAGGTTATTGATATAGAAACCCAGCATAGATAACTTTTCCACAGCTGGATATAACCT	984
Qy	220	GAATCCCATAGAGGAACTGTGGAAATTAAAAATGTTTCITTCAAATTATCCATCAAGACCA	279
Db	985	GAATCCCATAGAGGAACTGTGGAAATTAAAAATGTTTCITTCAAATTATCCATCAAGACCA	1044
Qy	280	TCTATCAAGATCTCGAAGGCTCTCAATCTCAGAAATTAAAGTCTGAGAGAGACAGTCGCCCTTG	339
Db	1045	TCTATCAAGATCTCGAAGGCTCTCAATCTCAGAAATTAAAGTCTGAGAGAGACAGTCGCCCTTG	1104
Qy	340	GTCGGTCTCAATGSCATGCGGAAGAGTACGGTAGTCCAGCTTCTGCGAGAGTTATATGAT	399
Db	1105	GTCGGTCTCAATGSCATGCGGAAGAGTACGGTAGTCCAGCTTCTGCGAGAGTTATATGAT	1164
Qy	400	CCGCAATGATGGCTTTATCATGGTGCATGAGAAATGACATCAGAGCTTTAAATGTGCGGCAT	459
Db	1165	CCGCAATGATGGCTTTATCATGGTGCATGAGAAATGACATCAGAGCTTTAAATGTGCGGCAT	1224
Qy	460	TATCGAGACCAATTATGGAGTGGTTAGTCAAGAGCCTGTTTGTTCGGGACCAACATCAGT	519
Db	1225	TATCGAGACCAATTATGGAGTGGTTAGTCAAGAGCCTGTTTGTTCGGGACCAACATCAGT	1284
Qy	520	AACAAATATCAAGTATGGAAGAGATGATCTGACTGATGAAGAGATGGAGAGAGCAGCAAGG	579

2365	CTGATTCTGAGTATTGCTCCAGTACTTGCCTGTGACAGGAAATGATTTGAAACCGCAGCAATG	2422
1660	ACTGGATTTGCCAAACAAAGATTAAGCAAGAACTTAAGCATGCTCGGAAGATAGCAACTGAA	1719
2425	ACTGGATTTGCCAAACAAAGATTAAGCAAGAACTTAAGCATGCTCGGAAGATAGCAACTGAA	2484
1720	GCCTTTGCGAATATACGTACTATAGTGTCACTAAACAAGGGAAGAAAGCCTTCGAGCAAAATG	1779
2485	GCCTTTGCGAATATAGTACTATAGTGTCACTAAACAAGGGAAGAAAGCCTTCGAGCAAAATG	2544
1780	TATGAAGAGATGCTTTCAGACTCAACACAGAAATACCTCGAAGAAAGCACAGATTAATGGA	1839
2545	TATGAAGAGATGCTTTCAGACTCAACACAGAAATACCTCGAAGAAAGCACAGATTAATGGA	2604
1840	AGCTGTATGCAATTGAGCCATGCGCATTCCTATATTTTGGCTATGCGACAGGGTTTCGATTT	1899
2605	AGCTGTATGCAATTGAGCCATGCGCATTCCTATATTTTGGCTATGCGACAGGGTTTCGATTT	2664
1900	GGAGCCTATTAAATTCAGCTGGAGGAATGACCCAGAGGGGCATGTTTCAATAGTTTTTACT	1959
2665	GGAGCCTATTAAATTCAGCTGGAGGAATGACCCAGAGGGGCATGTTTCAATAGTTTTTACT	2724
1960	GCAATTCGATATGGAAGCTATAGGCCATCGGAAAAAGCTCGCTTTGGCTCCTGAAATATTC	2019
2725	GCAATTCGATATGGAAGCTATAGGCCATCGGAAAAAGCTCGCTTTGGCTCCTGAAATATTC	2784
2020	AAAGCCAAATCGGGGCTGCGCATCTGTTTGGCTTGTTCGAAAAAGAAACCAATATAGAC	2079
2785	AAAGCCAAATCGGGGCTGCGCATCTGTTTGGCTTGTTCGAAAAAGAAACCAATATAGAC	2844
2080	AGCCGAGTCAAGAAAGGAAAAAGCCAGACACATGTGAAGGAAATTTAGAGTTTCAGAA	2139
2845	AGCCGAGTCAAGAAAGGAAAAAGCCAGACACATGTGAAGGAAATTTAGAGTTTCAGAA	2904
2140	GTCTCTTCTCTATNCATGTCGCCCGAGATGTTTTTCATCTCCGTGGCTTATCCCTCAGT	2199
2905	GTCTCTTCTCTATNCATGTCGCCCGAGATGTTTTTCATCTCCGTGGCTTATCCCTCAGT	2964
2200	ATTGAGCGAGAAAGACAGTAGTACATTTGTGGGAGCAGCGGCTGTGGGAAAAAGCACTTCT	2259
2965	ATTGAGCGAGAAAGACAGTAGTACATTTGTGGGAGCAGCGGCTGTGGGAAAAAGCACTTCT	3024
2260	GTTCACATCTCCAGACACTTATGACCCCGTGAAGGACAGTCTGTTTCATGGTGTG	2319
3025	GTTCACATCTCCAGACACTTATGACCCCGTGAAGGACAGTCTGTTTCATGGTGTG	3084
2320	GATGCAAAAGAAATTCGAATGACAGTGGTCCGTTCCCAAATAGCAATCGTTCCCTCAAGAG	2379
3085	GATGCAAAAGAAATTCGAATGACAGTGGTCCGTTCCCAAATAGCAATCGTTCCCTCAAGAG	3144
2380	CCTGTGCTCTTCACTGACAGCAATGCTGAGAAACATGGCTATATGGTGAACAGCCGTGTG	2439
3145	CCTGTGCTCTTCACTGACAGCAATGCTGAGAAACATGGCTATATGGTGAACAGCCGTGTG	3204
2440	GTGCCATTAGATGAGATCAAGAGCCGCAATGACGAAATATCATTTCTTTTATTCGA	2499
3205	GTGCCATTAGATGAGATCAAGAGCCGCAATGACGAAATATCATTTCTTTTATTCGA	3264
2500	GGTCTCCCTGAGAAATACAACAACAAGTTGCACTGAAAGGAGCAAGCTTTCTGCGCGC	2559
3265	GGTCTCCCTGAGAAATACAACAACAAGTTGCACTGAAAGGAGCAAGCTTTCTGCGCGC	3324
2560	CAGAAACAAAGACTAGCTATTGCAAGGCTCTTCTCCAAAACCCAAATTTTATTTGTG	2619
3325	CAGAAACAAAGACTAGCTATTGCAAGGCTCTTCTCCAAAACCCAAATTTTATTTGTG	3384
2620	GATGAGGCCACTTTCAGCCCTCGATTAATGACAGTGAAGAGTGGTTTCAGATGCCCTTGAT	2679
3385	GATGAGGCCACTTTCAGCCCTCGATTAATGACAGTGAAGAGTGGTTTCAGATGCCCTTGAT	3444
2680	AAAGCCAGGACGGGAAGGACATGCTCTAGTGGTCACTCAGAGCTCTCTGCAATTCAGAC	2739
3445	AAAGCCAGGACGGGAAGGACATGCTCTAGTGGTCACTCAGAGCTCTCTGCAATTCAGAC	3504

QY 2740 GCAGATTGATAGTGGTCTGACAAATGGAAGATGAAAGGACAGGAACATCATCAAGAG 2799
DB 3505 GCAGATTGATAGTGGTCTGACAAATGGAAGATGAAAGGACAGGAACATCATCAAGAG 3564
QY 2800 CTCCTGAGAAATCGAGACATATATTTAAAGTTAGTGAATGACAGTCAAGTCAAGTGA 2856
DB 3565 CTCCTGAGAAATCGAGACATATATTTAAAGTTAGTGAATGACAGTCAAGTCAAGTGA 3621

RESULT 4
US-09-873-409-13
; Sequence 13, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 13
; LENGTH: 3702
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: No. US20020037522A1
; LOCATION: (723)...(723)
; OTHER INFORMATION: n at position 723 represents any nucleotide (A, T, C or G)

US-09-873-409-13

Query Match 94.2%; Score 2690.6; DB 9; Length 3702;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2693; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 160 TCCCTCATTTGATAAGAAACCCAGTATAGATAAATTTCCACAGCTGGATATAAACCT 219
DB 1006 TCCAGGTATTTGATAAGAAACCCAGTATAGATAAATTTCCACAGCTGGATATAAACCT 1065

QY 220 GAATCCATAGAGGAACTGTGAATTTAAATGTTCTTCAATATCCATCAAGACCA 279
DB 1066 GAATCCATAGAGGAACTGTGAATTTAAATGTTCTTCAATATCCATCAAGACCA 1125

QY 280 TCTATCAAGATTTCTGAAGGTTCTGAATCTCAGAAATTAAGTCTGGAGACAGTGCCTTG 339
DB 1126 TCTATCAAGATTTCTGAAGGTTCTGAATCTCAGAAATTAAGTCTGGAGACAGTGCCTTG 1185

QY 340 GTCCGTCTCAATGGCAGTGGGAGAGTACGTTAGTCCAGCTTCTCCAGAGGTTATATGAT 399
DB 1186 GTCCGTCTCAATGGCAGTGGGAGAGTACGTTAGTCCAGCTTCTCCAGAGGTTATATGAT 1245

QY 400 CCGGATGATGGCTTTATCATGTGGATGAGATGACATCAGAGCTTTAAATGTGGGCAAT 459
DB 1246 CCGGATGATGGCTTTATCATGTGGATGAGATGACATCAGAGCTTTAAATGTGGGCAAT 1305

QY 460 TATCGAGACCATATTTGGAGTGTATAGTCAAGAGCTTTTGTTCGGACCAACATCAGT 519
DB 1306 TATCGAGACCATATTTGGAGTGTATAGTCAAGAGCTTTTGTTCGGACCAACATCAGT 1365

QY 520 AACAAATATCAAGTATGAGAGATGATGTACTGATGAAGAGATGAGAGAGCAGCAGG 579
DB 1366 AACAAATATCAAGTATGAGAGATGATGTACTGATGAAGAGATGAGAGAGCAGCAGG 1425

QY 580 GAAGCAATATGATATTTATCATGGAGTTTCTTAATAATTTAAATATGATTTGGTAGGG 639
DB 1426 GAAGCAATATGATATTTATCATGGAGTTTCTTAATAATTTAAATATGATTTGGTAGGG 1485

QY 640 GAAGAAGGCTCAATGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 699
DB 1486 GAAGAAGGAGCTCAATGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1545

QY 700 GTTCGAAACCCCAAGATTTCTGATTTTAGATGAGGCTACGTTCTGCCCTCGGATTCAGAAAGC 759
DB 1546 GTTCGAAACCCCAAGATTTCTGATTTTAGATGAGGCTACGTTCTGCCCTCGGATTCAGAAAGC 1605

QY 760 AAGTCAGCTGTTCAGGCTGCACTGGAGAGCCAGCAAGCTCGGACTACAAATCGTGTA 819
DB 1506 AAGTCAGCTGTTCAGGCTGCACTGGAGAGCCAGCAAGCTCGGACTACAAATCGTGTA 1665

QY 820 GCACACCGACTTTCTACTATTTCGAAGTCAGATTTGATTTGTGACCTCCCTAAAGATGGAATG 879
DB 1666 GCACACCGACTTTCTACTATTTCGAAGTCAGATTTGATTTGTGACCTCCCTAAAGATGGAATG 1725

QY 880 CTGCGGAGAGAAAGGAGCAGATCTGTAACCTAATGSCAAAACGAGCTCTATATTTACTTT 939
DB 1726 CTGCGGAGAGAAAGGAGCAGATCTGTAACCTAATGSCAAAACGAGCTCTATATTTACTTT 1785

QY 940 GTGATGTCACAGGATATTAATAAAGCTGATGAACAGATGAGTCAATGACATATTTACT 999
DB 1786 GTGATGTCACAGGATATTAATAAAGCTGATGAACAGATGAGTCAATGACATATTTACT 1845

QY 1000 GAAAGAAAGACCAACTCACCTTCCTGCACTCTGTGGAAGAGCATCAAGTCAGACTTCATT 1059
DB 1846 GAAAGAAAGACCAACTCACCTTCCTGCACTCTGTGGAAGAGCATCAAGTCAGACTTCATT 1905

QY 1060 GACAAGGCTGAGGAATCCACCCTAATCTAAAGAGATAGTCTTCTCTGAAGTCTCTCTATTA 1119
DB 1906 GACAAGGCTGAGGAATCCACCCTAATCTAAAGAGATAGTCTTCTCTGAAGTCTCTCTATTA 1965

QY 1120 AATAATTTAAAGTTAAACAGCCTGTAATGCGCTTTTGTGCTGCGGACATTTGGCTCT 1179
DB 1966 AATAATTTAAAGTTAAACAGCCTGTAATGCGCTTTTGTGCTGCGGACATTTGGCTCT 2025

QY 1180 GTTCTAAATGGAACCTGTTCATCCAGTATTTTCCATCATCTTTTCCAAAAATTTAAACCATG 1239
DB 2026 GTTCTAAATGGAACCTGTTCATCCAGTATTTTCCATCATCTTTTCCAAAAATTTAAACCATG 2085

QY 1240 TTTGGAATTAATGATAAAACCAATTAAGCATGATGCGAAATTTATTTCCATGATATTC 1299
DB 2086 TTTGGAATTAATGATAAAACCAATTAAGCATGATGCGAAATTTATTTCCATGATATTC 2145

QY 1300 GTCAATTTGGGTGTATTTCTGCTTTGTTCAGTATTTTCATGAGGATTTATTTACGGCAGA 1359
DB 2146 GTCAATTTGGGTGTATTTCTGCTTTGTTCAGTATTTTCATGAGGATTTATTTACGGCAGA 2205

QY 1360 GCAGGGAAATTTTAACGATGAGATTAAGACACTTGGCTTCCAAAGCCATGTTATATCAG 1419
DB 2206 GCAGGGAAATTTTAACGATGAGATTAAGACACTTGGCTTCCAAAGCCATGTTATATCAG 2265

QY 1420 GATATTCCTGCTGTTGATGAAAGGAAACAGCACAGGAGCTTGAACAATATTAGCC 1479
DB 2266 GATATTCCTGCTGTTGATGAAAGGAAACAGCACAGGAGCTTGAACAATATTAGCC 2325

QY 1480 ATAGATATAGCACAAATTTCAAGGAGCAACAGGTTCCAGGATTTGGCGTTTAAACACAAAT 1539
DB 2326 ATAGATATAGCACAAATTTCAAGGAGCAACAGGTTCCAGGATTTGGCGTTTAAACACAAAT 2385

QY 1540 GCAACTAAATGAGGACTTTTCAGTTATCATCTTCTTTATATATGATGAGGAGATGACATTC 1599
DB 2386 GCAACTAAATGAGGACTTTTCAGTTATCATCTTCTTTATATATGATGAGGAGATGACATTC 2445

QY 1600 CTGATTCGAGTATTTGCTCCAGTACTTGGCGTGAAGAGATGATTTGAACCCGAGCAATG 1659
DB 2446 CTGATTCGAGTATTTGCTCCAGTACTTGGCGTGAAGAGATGATTTGAACCCGAGCAATG 2505

QY 1660 ACTGGATTTGCCAAACAAAGATAGCAAGATCTTAAGCATCTGGAAGATAGCAACTGAA 1719
DB 2506 ACTGGATTTGCCAAACAAAGATAGCAAGATCTTAAGCATCTGGAAGATAGCAACTGAA 2565

QY 1720 GCTTTGGAGATATACGTAATGATGCTTAAAGGAGGAAAGGCTTTCGAGCAAAATG 1779
DB 2566 GCTTTGGAGATATACGTAATGATGCTTAAAGGAGGAAAGGCTTTCGAGCAAAATG 2625

1780 QY TATGAGAGATGCTTACAGCTCAACACAGAAATACCTCGAAGAAAGCACAGATTATTGGA 1839
 2626 Db TATGAGAGATGCTTACAGCTCAACACAGAAATACCTCGAAGAAAGCACAGATTATTGGA 2685
 1840 QY AGCTGTTATGCAATTCAGCCATGCTTTATATATTTTGGCTATGCGAGGGTTTCGATTT 1899
 2686 Db AGCTGTTATGCAATTCAGCCATGCTTTATATATTTTGGCTATGCGAGGGTTTCGATTT 2745
 1900 QY GAGGCTTATTAAATCAAGCTGAGCAATGACCCAGAGGGCAATGTTCAATGTTTACT 1959
 2746 Db GAGGCTTATTAAATCAAGCTGAGCAATGACCCAGAGGGCAATGTTCAATGTTTACT 2805
 1960 QY GCAATTCATATGAGGATATGCGCATCGGAATAACCGCTCTTTGGCTCTCGAATATCC 2019
 2806 Db GCAATTCATATGAGGATATGCGCATCGGAATAACCGCTCTTTGGCTCTCGAATATCC 2865
 2020 QY AAAGCCAAATCGGGGCTGGCATCTCTTTGGCTTTGTGAAAGAAACCAATATAGAC 2079
 2866 Db AAAGCCAAATCGGGGCTGGCATCTCTTTGGCTTTGTGAAAGAAACCAATATAGAC 2925
 2080 QY AGCGGAGTCAAGAGGAAAGGACAGACATGTAAGGGATTTAGAGTTTCAGAA 2139
 2926 Db AGCGGAGTCAAGAGGAAAGGACAGACATGTAAGGGATTTAGAGTTTCAGAA 2985
 2140 QY GTCTCTTCTTCTATCCATGTGCGCCAGATGTTTTCATCTCGTGGCTTATCCCTCAGT 2199
 2986 Db GTCTCTTCTTCTATCCATGTGCGCCAGATGTTTTCATCTCGTGGCTTATCCCTCAGT 3045
 2200 QY ATTGAGGAGAAAGACAGTAGCAATTTGTGGGAGCAGCGCTGTGGGAAAGCACTTCT 2259
 3046 Db ATTGAGGAGAAAGACAGTAGCAATTTGTGGGAGCAGCGCTGTGGGAAAGCACTTCT 3105
 2260 QY GTTCAACTCTGACAGACATTTATGACCCGTGCAAGCAAGTGTGTTGATGTTG 2319
 3106 Db GTTCAACTCTGACAGACATTTATGACCCGTGCAAGCAAGTGTGTTGATGTTG 3165
 2320 QY GATCAAAAGAAATGAATGACAGTGGCTCGTTTCCCAATAGCAATTCGTTCTCAAGAG 2379
 3166 Db GATCAAAAGAAATGAATGACAGTGGCTCGTTTCCCAATAGCAATTCGTTCTCAAGAG 3225
 2380 QY CCTGTGCTTCACTGACGATGCTGAGCAATCGCCTATGTTGACACAGCGCTG 2439
 3226 Db CCTGTGCTTCACTGACGATGCTGAGCAATCGCCTATGTTGACACAGCGCTG 3285
 2440 QY GTGCAATTAGATGATCAAGAGCGCAATGACAGCAATATCCATTTCTTTATTGAA 2499
 3286 Db GTGCAATTAGATGATCAAGAGCGCAATGACAGCAATATCCATTTCTTTATTGAA 3345
 2500 QY GGTCTCCTGAGAAATACACACAAAGTTGGACTGAAAGGACAGAGCTTCTGGCGGC 2559
 3346 Db GGTCTCCTGAGAAATACACACAAAGTTGGACTGAAAGGACAGAGCTTCTGGCGGC 3405
 2560 QY CAGAAACAAAGACTAGCTATTGCAAGGCTCTTCTCCAAAACCCAAAATTTTATTGTTG 2619
 3406 Db CAGAAACAAAGACTAGCTATTGCAAGGCTCTTCTCCAAAACCCAAAATTTTATTGTTG 3465
 2620 QY GATGAGGCCACTCAGCCCTCGAATGACAGTGAAGAGTGTGTTCAAGATGCCCCTTGAT 2679
 3466 Db GATGAGGCCACTCAGCCCTCGAATGACAGTGAAGAGTGTGTTCAAGATGCCCCTTGAT 3525
 2680 QY AAAGCCAGGCGGAGGACATGCTAGTGTGCTACTCAGAGGCTCTCTGCAATTCAGAAC 2739
 3526 Db AAAGCCAGGCGGAGGACATGCTAGTGTGCTACTCAGAGGCTCTCTGCAATTCAGAAC 3585
 2740 QY GCAGATTGATGATGTTTCTGCAATGGAAGATAAAGGAAACAAAGGAACTCATCAAGAG 2799
 3586 Db GCAGATTGATGATGTTTCTGCAATGGAAGATAAAGGAAACAAAGGAACTCATCAAGAG 3645
 2800 QY CTCTGAGAAATCAGACATATATTTTAAAGTTAGTGAATGACAGAGTCAAGTCAAGTGA 2856
 3646 Db CTCTGAGAAATCAGACATATATTTTAAAGTTAGTGAATGACAGAGTCAAGTCAAGTGA 3702

RESULT 5
 US-10-415-378-34
 : Sequence 34, Application US/10415378
 : Publication No. US20040014945A1
 : GENERAL INFORMATION:
 : APPLICANT: INCYTE CORPORATION; TANG, Y. Tom
 : APPLICANT: YOE, Henry; NGUYEN, Damien B.;
 : APPLICANT: HAFALIA, April J.A.; ELLIOTT, Vicki S.;
 : APPLICANT: LU, Yan; CHAMLA, Narinder K.;
 : APPLICANT: YAO, Monique G.; BAUGHEN, Mariah R.;
 : APPLICANT: GANDHI, Ameena R.; DING, Li;
 : APPLICANT: SANTANWALA, Madhusudan M.; RAMKUMAR, Jayalaxmi;
 : APPLICANT: ARVIZU, Chandra S.; GIETZEN, Kimberly J.;
 : APPLICANT: LAL, Preeti G.; AZIMZAI, Yalda;
 : APPLICANT: KHAN, Farran A.; THANGAVELU, Kavitha;
 : APPLICANT: THROBTON, Michael B.; LU, Dyrung Aina M.;
 : APPLICANT: TRIBOULEY, Catherine M.; WARREN, Bridget A.;
 : APPLICANT: ISON, H. Craig; DAS, Debopriya;
 : APPLICANT: RAUMANN, Brigitte E.; POLICKY, Jennifer L.;
 : APPLICANT: KEARNEY, Liam
 : TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
 : FILE REFERENCE: PI-0270 USN
 : CURRENT APPLICATION NUMBER: US/10/415,378
 : CURRENT FILING DATE: 2003-05-07
 : PRIOR APPLICATION NUMBER: PCT/US01/46055
 : PRIOR FILING DATE: 2001-10-27
 : PRIOR APPLICATION NUMBER: US 60/250,790
 : PRIOR FILING DATE: 2000-12-01
 : PRIOR APPLICATION NUMBER: US 60/252,232
 : PRIOR FILING DATE: 2000-11-20
 : PRIOR APPLICATION NUMBER: US 60/249,661
 : PRIOR FILING DATE: 2000-11-17
 : PRIOR APPLICATION NUMBER: US 60/247,673
 : PRIOR FILING DATE: 2000-11-09
 : PRIOR APPLICATION NUMBER: US 60/245,904
 : PRIOR FILING DATE: 2000-11-03
 : PRIOR APPLICATION NUMBER: US 60/243,989
 : PRIOR FILING DATE: 2000-10-27
 : NUMBER OF SEQ ID NOS: 40
 : SOFTWARE: PERL Program
 : SEQ ID NO 34
 : LENGTH: 3699
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : NAME/KEY: misc feature
 : OTHER INFORMATION: Incyte ID No. US20040014945A1 7472030CB1
 US-10-415-378-34

Query Match 88.1%; Score 2515; DB 16; Length 3699;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 2609; Conservative 0; Mismatches 10; Indels 78; Gaps 1;
 QY 160 TCCTCATTTATGATAAGAACCCAGTATAGATACTTTCCACAGCTGGATATAACCT 219
 Db 1081 TTCAGGTTATTGATAGAAACCCAGTATAGTTAACTTTCCACAGCTGGATATAACCT 1140
 QY 220 GAATCCATAGAAGAACTGTGGAATTTAAAAATGTTCTTCAATTTATCCATCAAGACCA 279
 Db 1141 GAATCCATAGAAGAACTGTGGAATTTAAAAATGTTCTTCAATTTATCCATCAAGACCA 1200
 QY 280 TCTATCAAGATTTGAAAGCTCTGAATCTCAGATTAAGCTCTGGAGAGCAGTCGCTTG 339
 Db 1201 TCTATCAAGATTTGAAAGCTCTGAATCTCAGATTAAGCTCTGGAGAGCAGTCGCTTG 1260
 QY 340 GTGGTCTCAATGGCAGTGGGAAGAGTACGGTAGTCCAGCTTCTGCAGAGGTTATATGAT 399
 Db 1261 GTGGTCTCAATGGCAGTGGGAAGAGTACGGTAGTCCAGCTTCTGCAGAGGTTATATGAT 1320
 QY 400 CCGGATGATGGCTTTATCATGTTGGATGAGATGATCATCAGAGCTTTAAATGTGGGCAAT 459
 Db 1321 CCGGATGATGGCTTTATCATGTTGGATGAGATGATCATCAGAGCTTTAAATGTGGGCAAT 1380

QY 460 TATCAGACCATATTTGGAGTGGTTAGTCAAGAGCCTGTTTTGTTCCGGACCCACCATCAGT 519
DB 1381 TATCGAGACCATATTTGGAGTGGTTAGTCAAGAGCCTGTTTTGTTCCGGACCCACCATCAGT 1440
QY 520 AACAAATCAAGTATGGAAGAGATGATGTGCTGATCAAGAGATGGAAGAGAGCAGCAAGG 579
DB 1441 AACAAATCAAGTATGGAAGAGATGATGTGCTGATCAAGAGATGGAAGAGAGCAGCAAGG 1500
QY 580 GAAGCAAAATGCGTATGATTTTATCATGCGAGTTTCTTAATAAAATTAATACATTTGGTAGGG 639
DB 1501 GAAGCAAAATGCGTATGATTTTATCATGCGAGTTTCTTAATAAAATTAATACATTTGGTAGGG 1560
QY 640 GAAAGAGAGAGCTCAAAATGAGTGGAGGCGAGAAACAGAGGATGCGAAATTTGCTGCGCTTAA 699
DB 1561 GAAAGAGAGAGCTCAAAATGAGTGGAGGCGAGAAACAGAGGATGCGAAATTTGCTGCGCTTAA 1620
QY 700 GTTCGAACCCCAAGATTCGATTTTATCATGCGAGTTTCTTAATAAAATTAATACATTTGGTAGGG 759
DB 1621 GTTCGAACCCCAAGATTCGATTTTATCATGCGAGTTTCTTAATAAAATTAATACATTTGGTAGGG 1680
QY 760 AAGTCAGCTGTTCAAGCTGCACTGGAGAGGCGAGCAAAAGGTGCGAATTCGAATCGTGGA 819
DB 1681 AAGTCAGCTGTTCAAGCTGCACTGGAGAGGCGAGCAAAAGGTGCGAATTCGAATCGTGGA 1740
QY 820 GCACACCGACCTTCTACTATTCGAAGTGCAGATTTGATTTGACCTTAAGAGATGGAATG 879
DB 1741 GCACACCGACCTTCTACTATTCGAAGTGCAGATTTGATTTGACCTTAAGAGATGGAATG 1800
QY 880 CTGGCGGAGAAAGAGACATGCTGCACTAATGCAAAACGAGGTCTATATTAATTCACIT 939
DB 1801 CTGGCGGAGAAAGAGACATGCTGCACTAATGCAAAACGAGGTCTATATTAATTCACIT 1860
QY 940 GTGATGTCACAGGATATTAATAAAGCTGATGAAACAGATGGAATCAATGACATTTCTACT 999
DB 1861 GTGATGTCACAGGATATTAATAAAGCTGATGAAACAGATGGAATCAATGACATTTCTACT 1920
QY 1000 GAAAGAAAGACCAATCACTTCTCTGTCGACCTCTGTAAGAGCATCAAGTCAGACTTCAT 1059
DB 1921 GAAAGAAAGACCAATCACTTCTCTGTCGACCTCTGTAAGAGCATCAAGTCAGACTTCAT 1080
QY 1060 CACAAGGCTGAGGAATCCACCAATCTAAAGAGATAAGTCTTCTGAAAGTCTCTCTATTA 1119
DB 1981 CACAAGGCTGAGGAATCCACCAATCTAAAGAGATAAGTCTTCTGAAAGTCTCTCTATTA 2040
QY 1120 AAAATTTTAAAGTTAAACAGCCTGAATGGCCTTTGCTGTTCTGGGAGCATTTGGCTTCT 1179
DB 2041 AAAATTTTAAAGTTAAACAGCCTGAATGGCCTTTGCTGTTCTGGGAGCATTTGGCTTCT 2100
QY 1180 GTTCTAAATGGAACCTGTTTATCCAGTATTTTCCATCATCTTTGCAAAATTTATAACCATG 1239
DB 2101 GTTCTAAATGGAACCTGTTTATCCAGTATTTTCCATCATCTTTGCAAAATTTATAACCATG 2160
QY 1240 TTTGGAATTAATGATAAAACCAATTAAGCATGATGAGAGAAATTTATTCATGATTTTC 1299
DB 2161 TTTGGAATTAATGATAAAACCAATTAAGCATGATGAGAGAAATTTATTCATGATTTTC 2220
QY 1300 GTCAATTTGGGCTGTTATTTGCTTTGTCAGTTATTTCTAGGGGATTTATTTAAGGCAGA 1359
DB 2221 GTCAATTTGGGCTGTTATTTGCTTTGTCAGTTATTTCTAGTTATTTCTAGT 2259
QY 1360 GCAGGGGAAATTTTAAACGATGAGATTAAGACACTTTGGCTTCAAGCCATGTTATATTCAG 1419
DB 2260 -----CAG 2262
QY 1420 GATATTGCTGCTTTGATGAAAGGAAACAGACAGAGCCTTGACAAACATATTTAGCC 1479
DB 2263 GATATTGCTGCTTTGATGAAAGGAAACAGACAGAGCCTTGACAAACATATTTAGCC 2322
QY 1480 ATAGATATGACAAATTTCAAGGAGCAACAGTTTCCAGGATTTGGCGTCTTAAACAAAT 1539
DB 2323 ATAGATATGACAAATTTCAAGGAGCAACAGTTTCCAGGATTTGGCGTCTTAAACAAAT 2382
QY 1540 GCAACTACATGGGACCTTTTCAGTTATCATTTCTTTATATGATGGAGATGACATTC 1599

DB 2383 GCNACTTAACATGGGACTTTTCAGTTATCATTTCTTTATATATGATGGAGATGACATTC 2442
QY 1600 CTGATTTCTGAGTATTTGCTCCAGTACTTTGCGGTGACAGGAATGATTTGAACCCGACGAATG 1659
DB 2443 CTGATTTCTGAGTATTTGCTCCAGTACTTTGCGGTGACAGGAATGATTTGAACCCGACGAATG 2502
QY 1660 ACTGGATTTTCCAAACAAAGATTAAGCAAGAACTTAAGCATGCTGGAAAGATAGCAACTGAA 1719
DB 2503 ACTGGATTTTCCAAACAAAGATTAAGCAAGAACTTAAGCATGCTGGAAAGATAGCAACTGAA 2562
QY 1720 GCTTTTCGAGAAATATACGTACTATAGTGTCAATTAACAAAGGAAAGAAAGCCTTTGAGGAAATG 1779
DB 2563 GCTTTTCGAGAAATATACGTACTATAGTGTCAATTAACAAAGGAAAGAAAGCCTTTGAGGAAATG 2622
QY 1780 TATGAGAGAGATGCTTCAGAGACTCAACACAGAAATACCTCGAAGAAAGACACAGATTTATGGA 1839
DB 2623 TATGAGAGAGATGCTTCAGAGACTCAACACAGAAATACCTCGAAGAAAGACACAGATTTATGGA 2682
QY 1840 AGCTGTTATGCAATTCAGCCATGCGCATGCTTTATATATTTGCTCTATGACAGAGGTTTCATTT 1899
DB 2683 AGCTGTTATGCAATTCAGCCATGCGCATGCTTTATATATTTGCTCTATGCGGACGGTTTCATTT 2742
QY 1900 GGAGCCTATTTAATTCAGCTGAGCAANTGACCCAGAGGCGATGTTTCATAGTTTACT 1959
DB 2743 GGAGCCTATTTAATTCAGCTGAGCAANTGACCCAGAGGCGATGTTTCATAGTTTACT 2802
QY 1960 GCAATTTGCATATGAGACTATGCGCATGCGAAAGAGCTCGTTTGGCTCCTGAATATTC 2019
DB 2803 GCAATTTGCATATGAGACTATGCGCATGCGAAAGAGCTCGTTTGGCTCCTGAATATTC 2862
QY 2020 AAGCCAAATTCGGGGCTCGGCATCTGTTGCTGCTGTTGGAAGAAAGAAACCAATATAGAC 2079
DB 2863 AAGCCAAATTCGGGGCTCGGCATCTGTTGCTGCTGTTGGAAGAAAGAAACCAATATAGAC 2922
QY 2080 AGCCGAGTCAAGAAAGGAGAAAGCCAGACACATGTAAGGGAAATTTAGAGTTTCGAGAA 2139
DB 2923 AGCCGAGTCAAGAAAGGAGAAAGCCAGACACATGTAAGGGAAATTTAGAGTTTCGAGAA 2982
QY 2140 GTCTCTTTCTTCTATTCATGTCGCCAGATGTTTTCATCCTCGTGCTTATTCCTCAGT 2199
DB 2983 GTCTCTTTCTTCTATTCATGTCGCCAGATGTTTTCATCCTCGTGCTTATTCCTCAGT 3042
QY 2200 ATTGACGAGGAAAGACAGTAGCATTTGTTGGGGAGCAGCGGCTGTGGGAAAGACACTTCT 2259
DB 3043 ATTGACGAGGAAAGACAGTAGCATTTGTTGGGGAGCAGCGGCTGTGGGAAAGACACTTCT 3102
QY 2260 GTTCAAATTCGACAGACTTTATGACCCCGTGCAGGCAAGTGTCTGTTGATGGTGTG 2319
DB 3103 GTTCAAATTCGACAGACTTTATGACCCCGTGCAGGCAAGTGTCTGTTGATGGTGTG 3162
QY 2320 GATGCAAAAGAAATTTGAATGTACAGTGGCTCCGTTCCAAATAGCAATCGTTCTCAAGAG 2379
DB 3163 GATGCAAAAGAAATTTGAATGTACAGTGGCTCCGTTCCAAATAGCAATCGTTCTCAAGAG 3222
QY 2380 CTTGTGCTCTTCAACTGACAGCATTTGCTGAGAAACATGCGCTATGTTGTCACAAAGCCGTGTG 2439
DB 3223 CTTGTGCTCTTCAACTGACAGCATTTGCTGAGAAACATGCGCTATGTTGTCACAAAGCCGTGTG 3282
QY 2440 GTGCAATTTAGATGAGATCAAGAGCCCAATGAGCAAAATATCCATTTCTTTATTTGAA 2499
DB 3283 GTGCAATTTAGATGAGATCAAGAGCCCAATGAGCAAAATATCCATTTCTTTATTTGAA 3342
QY 2500 GGTCTCCCTGAGAAATPACACACACAAGTTGGACTGAAAGGAGACAGCTTTCTGCGGC 2559
DB 3343 GGTCTCCCTGAGAAATPACACACACAAGTTGGACTGAAAGGAGACAGCTTTCTGCGGC 3402
QY 2560 CAGAAACAAAGACTAGCTATTTGCAAGGCTCTTCTCCAAAGCCCAAAATTTATTTGTTG 2619
DB 3403 CAGAAACAAAGACTAGCTATTTGCAAGGCTCTTCTCCAAAGCCCAAAATTTATTTGTTG 3462
QY 2620 GATGAGGCACTTTGAGCCTTCGATATGACAGTGAAGGAGGTTTTCAGCATGCTTGTAT 2679

Db 3463 GATGAGCCACTTCAGCCCTCGATAATACAGTCAGAGAAGGTGGTTTCAGCATGCCCTTGAT 3522
Qy 2680 AAAGCCAGGACGGGAAGCAGATCGTAGTGTCTCACTCAGAGGCTCTCTGCAATTCAGAAC 2739
Db 3523 AAAGCCAGGACGGGAAGCAGATCGTAGTGTCTCACTCAGAGGCTCTCTGCAATTCAGAAC 3582
Qy 2740 GCAGATTGATAGTGGTTCTGCACAAATGGAAGATAAAGAAACAAAGAACTCATCAAGAG 2799
Db 3583 GCAGATTGATAGTGGTTCTGCACAAATGGAAGATAAAGAAACAAAGAACTCATCAAGAG 3642
Qy 2800 CTCTGAGGAATCGAGACATATATTTAAAGTTAGTGAATCCACAGTCAGTGCAGTGA 2856
Db 3643 CTCTGAGGAATCGAGACATATATTTAAAGTTAGTGAATCCACAGTCAGTGCAGTGA 3699

RESULT 6
US-09-873-409-9
; Sequence 9, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Sayegh, Mohamed
; APPLICANT: Frank, Markus
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-409-9

Query Match 72.3%; Score 2066; DB 9; Length 2066;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2066; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 791 CGACAAAGTCGAGCTACATCTGTGTAGCAGACGACCTTCTACTATTGGAAGTCAG 850
Db 1 CGACAAAGTCGAGCTACATCTGTGTAGCAGACGACCTTCTACTATTGGAAGTCAG 60
Qy 851 ATTTGATTGACCTAAAGATGGAATGCTGGCGGAGAAAGAGACATGCTCAACTAA 910
Db 61 ATTTGATTGACCTAAAGATGGAATGCTGGCGGAGAAAGAGACATGCTCAACTAA 120
Qy 911 TGGCAAAACGAGGTCTATATTTATTCTGATGTGTCAGGATATTTAAAGAGCTGATG 970
Db 121 TGGCAAAACGAGGTCTATATTTATTCTGATGTGTCAGGATATTTAAAGAGCTGATG 180
Qy 971 AACAGATGGAGTCATGACATATTTCTACTGAAGAAAGACCACTCTCTCTGCACT 1030
Db 181 AACAGATGGAGTCATGACATATTTCTACTGAAGAAAGACCACTCTCTCTGCACT 240
Qy 1031 CTGTGAAGAGCATCAAGTCAGACTTCATTTGCAAGGCTGAGGAATCCACCAATCTTAAG 1090
Db 241 CTGTGAAGAGCATCAAGTCAGACTTCATTTGCAAGGCTGAGGAATCCACCAATCTTAAG 300
Qy 1091 AGATAAGTCTCTGAGTCTCTCTATTAAGATTTAAAGTTAAACAGCCTGAATGGC 1150
Db 301 AGATAAGTCTCTGAGTCTCTCTATTAAGATTTAAAGTTAAACAGCCTGAATGGC 360
Qy 1151 CTTTTGTGGTTCTGGGACATGCTCTCTGTTCTAAATGGAACCTGTTCACTCCAGTATTT 1210
Db 361 CTTTTGTGGTTCTGGGACATGCTCTCTGTTCTAAATGGAACCTGTTCACTCCAGTATTT 420
Qy 1211 CCATCACTTTGGAAAATTAACCATGTTTGAATATATGATAAACCACATTAAGC 1270
Db 421 CCATCACTTTGGAAAATTAACCATGTTTGAATATATGATAAACCACATTAAGC 480
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Db 481 ATGATGACAGAAATTTATTCATGATATTCGTCATTTTGGGTGTTATTTGCTTTGTGAGTT 540
Qy 1331 ATTTTCATGACAGGATTTATTTTACCGCAGACAGAGGGAATTTTAAACGATGAGATTAAGAC 1390
Db 541 ATTTTCATGACAGGATTTATTTTACCGCAGACAGAGGGAATTTTAAACGATGAGATTAAGAC 600
Qy 1391 ACTTGGCCCTTCAAGCCATGTTATATCAGGATATTTGCCCTGGTTTGTATGAAGAGAAACA 1450
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Qy 1451 GCACAGGAGCTTGACAAATATTTAGCCATAGATATAGCACAATTTCAAGGAGCAACAG 1510
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Qy 1511 GTTCCAGGATTCGCGTCTTAAACAATAATGCAACTAAACATGAGGACCTTTTCACTTATCATTT 1570
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Db 1141 CCCAGAGGCAATGTTTCATAGTTTTTACTGCAATTCGATATGAGCTATGCGCATCGGAA 1200
Qy 1991 AAACGCTCGTTTTTGGCTCTGAAATATTTCAAAGCCAAATCGGGGCTGCGCATCTCTTTG 2050
Db 1201 AAACGCTCGTTTTTGGCTCTGAAATATTTCAAAGCCAAATCGGGGCTGCGCATCTCTTTG 1260
Qy 2051 CCTTGTGGAAAGAAACCAATATAGACAGCGGAGTCAAGAGGGAAGAAAGCCAGACA 2110
Db 1261 CCTTGTGGAAAGAAACCAATATAGACAGCGGAGTCAAGAGGGAAGAAAGCCAGACA 1320
Qy 2111 CATGTGAAGGATTTAGAGTTTCGAGAGTCTCTTCTTCTTCTATCCATGTCGCCAGATG 2170
Db 1321 CATGTGAAGGATTTAGAGTTTCGAGAGTCTCTTCTTCTTCTATCCATGTCGCCAGATG 1380
Qy 2171 TTTTCATCTCTCGTGGCTTATCCCTCAGTATTTGAGCGAGGAAAGACAGTAGCATTTGTGG 2230
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Qy 2231 GGAGCGGCTGTGGGAAAGACATCTCTTCACTCTCGAGAGACTTTATGACCCCG 2290
Db 1441 GGAGCGGCTGTGGGAAAGACATCTCTTCACTCTCGAGAGACTTTATGACCCCG 1500
Qy 2291 TGCAGACAAAGTGTCTGTTTGTGATGTTGATGATGATGATGATGATGATGATGATGATGATG 2350
Db 1501 TGCAGACAAAGTGTCTGTTTGTGATGTTGATGATGATGATGATGATGATGATGATGATGATG 1560
Qy 2351 GTTCCCAAAATAGCAATGTTTCTCAAGAGCTGTGTCTTCAATCTGACGATTTGCTGAGA 2410
Db 1561 GTTCCCAAAATAGCAATGTTTCTCAAGAGCTGTGTCTTCAATCTGACGATTTGCTGAGA 1620

QY 2411 ACATCGCCTATGGTGACACAGCGTGTGGTCCATTAGATGAGATCAAGAGCGCGCAA 2470
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QY 2471 ATGAGCAAAATATCCATCTTTTATTGAAGGTCTCCCTGAGAAATACACACAAAGTTG 2530
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QY 2531 GACTGAAAGGAGCAGCAGCTTTCTGCGGCCAGAAACAAAGACTAGCTATTGCAAGGCTC 2590
Db 1741 GACTGAAAGGAGCAGCAGCTTTCTGCGGCCAGAAACAAAGACTAGCTATTGCAAGGCTC 1800
QY 2591 TTCTCCAAAACCCCAAAATTTTATTGTTGGATGAGGCCACTTCAGCCCTCGATTAATGACA 2650
Db 1801 TTCTCCAAAACCCCAAAATTTTATTGTTGGATGAGGCCACTTCAGCCCTCGATTAATGACA 1860
QY 2651 GTGGAAGGTGTTTCCAGCATGCGCTTTGATAAGCCAGGAGCGGAGGACATGCTAGTGG 2710
Db 1861 GTGGAAGGTGTTTCCAGCATGCGCTTTGATAAGCCAGGAGCGGAGGACATGCTAGTGG 1920
QY 2711 TCACATCAGAGCTCTCTGCAATTCAGAACGCGAGATTTGATAGTGTCTGACAAATGAAA 2770
Db 1921 TCACATCAGAGCTCTCTGCAATTCAGAACGCGAGATTTGATAGTGTCTGACAAATGAAA 1980
QY 2771 AGATAAGGACAAAGGACATGATGAGAGCTCTGAGAAATCGAGACATATTTTAAGT 2830
Db 1981 AGATAAGGACAAAGGACATGATGAGAGCTCTGAGAAATCGAGACATATTTTAAGT 2040
QY 2831 TAGTGAATGCACAGTCAGTCAGTGA 2856
Db 2041 TAGTGAATGCACAGTCAGTCAGTGA 2066

RESULT 7
US-10-092-900A-303
; Sequence 303, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padisaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Kieper, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A

; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 303
; LENGTH: 4091
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)..(4078)
US-10-092-900A-303
Query Match 58.0%; Score 1657.2; DB 13; Length 4091;
Best Local Similarity 78.0%; Pred. No. 0;
Matches 2219; Conservative 0; Mismatches 508; Indels 117; Gaps 14;
QY 115 TTTTCTTTAGTGTAAATCCATAGCAGTTATTGCAATGAGAGCAGTCCCTCATTTATGAT 174
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QY 175 AAGAAACCCAGTATAGATTAATTTCCACAGCTGATATAAACCC-----TGAATCCATA 228
Db 1132 AAGAAACCAATATAGACGCCGAGTCAAGAGGAAAGACAGTAAGCGACATGT 1191
QY 229 GAAGGAACCTGTGGAATTTAAATTTTCTTTTCAATTTATCCATCAAGACCATCTATCAAG 288
Db 1192 GAAGGGAATTTAGAGTTTCGAGAAAGTCTCTTTCTCTATCCATGTCGCCAGATGTTTC 1251
QY 289 ATTCTGAAGGTCTGAATCTCAGATTTAGCTGGAGAGACACTGCGCTTGGTGGTCTC 348
Db 1252 ATCTTCGGTGGCTTTATCCCTCAGTATTGACGAGGAAAGACAGTAGCATTTGTGGGAGC 1311
QY 349 AATGGCAGTGGGAGAGTACGGTAGTCCAGCTTTCTGACAGGTTATATGATCCGAGATGAT 408
Db 1312 AGCGGCTGTGGAAAGACACTTCTGTTCAACTTTCTGACAGAGACTTTATGACCCCGTCAA 1371
QY 409 GGCTTTATCATGTGTGATGAGATGACATCAGAGCTTTAAATGTCGGCATTATCGAGAC 468
Db 1372 GG-----ACAAGTGGATGGTGTGGATGCAAAAGAAATTGAATGTACAGTGGCTCCGTTCC 1425
QY 469 CATATTGGAGTGGTTAGTCAAGAGCCCTGTTTGTTCGGGACCCACCACATCAGTAACAATATC 528
Db 1426 CAATAGCAATCGTTCTCTCAAGAGCCCTGCTCTTCACTGACAGCAATTGCTGGAACATC 1485
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QY 583 GCAATGCGTATGATTTTATCATGAGTTTCTTAATAAATTTTAAATACATTTGAGGGGAA 642
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QY 643 AAAGGAGCTCAAATGAGTGGAGGGGAGAAACAGAGGATCGCAATTTGCTGCTTAGTT 702

1606 AAAGGAGCACAGCTTTCTGGGGGCGAGAAACAAAGAGCTAGCTATTGCAAGGGCTCTTCTC 1665
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Db CAAAACCCCAAAATTTTATTTGTTGGATGAGGCCACTTCAGCCCTCGATATATGACAGTGAG 1725
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Qy GCACACGACCTTCTACTATTTGAGAGTGCAGATTTGATTTGACCCCTTAAGAGTGAATG 879
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Db ATAAAGGAACAAGGAATCTCATCAAGAGCTCTGAGAAATCGAGACATATATTTTAAAGTTA 1905
Qy GTGATGTCACAGGATATTAAGAAAGC----- 965
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Db ACATTTCTGATTCAGATATGCTCCAGTACTTGGCTGTCAGGATGATTTGAACGGA 2685
Qy GCAATGACTGGATTTGCCAAAGAGATAAGCAAGACTTAAGCATGCTGG-----AAAG 1707
Db |||||

Db 2686 GCAATGACTGGATTTTCCCAACAAAGATAAGCAAGAACTTTAAGCATGCTGGAAGGTTAAAG 2745
Qy 1708 ATAGCAACTGAAGCTTTGGAGATAATACGTACTATATAGTGTCTATTAACAAGGGAAGAACCC 1767
Db 2746 ATAGCAACTGAAGCTTTGGAGATAATACGTACTATATAGTGTCTATTAACAAGGGAAGAACCC 2805
Qy 1768 TTGAGCAAAATGATGAGAGATGCTTCAGACTCAACAC---AGAAATACCTCGAAGAAA 1824
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Db 2866 GCACAGATTTTGAAGCTGTTATGATTCAGCTCAGCCATGCTTTATATATTTTGTCTATGCG 2925
Qy 1885 GCAGGCTTTGATTTGAGGCTATTTAAATTCAGCTGAGCAAGATGACCCAGAGGGCATG 1944
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Qy 1945 TT---CATAGTTTCTGCAATTCGATTCAGCTATGAGCTATGCGCATCGGAAAGCGCTGTT 2001
Db 2986 TTTGATAGAGTTTCTGATTCGATTCGATTCAGCTATGAGCTATGCGCATCGGAAAGCGCTGTT 3045
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Db 3763 GTGGTCACTCAGAGGCTCTCTGCAATTCAGAAACGAGATTTGATAGTGTCTTGTGCAAT 3822

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QY      2767  GGAAGCATTAAGGAACAAGGAATCATCAAGAGCTCTCTGAGAAATCGAGACATATATTTT 2826
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Db      3823  GGAAGCATTAAGGAACAAGGAATCATCAAGAGCTCTCTGAGAAATCGAGACATATATTTT 3882
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QY      2827  AAGTTAGTGAATGCACAGTCAGTG 2850
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Db      3883  AAGTTAGTGAATGCACAGTCAGCG 3906
      |||

RESULT 8
US-09-805-020-30
; Sequence 30, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 4533
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(4533)
; OTHER INFORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-30

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Query Match	36.1%;	Score 1030.2;	DB 13;	Length 4533;
Best Local Similarity	62.3%;	Pred. No. 4e-269;		
Matches 1695;	Conservative 0;	Mismatches 988;	Indels 42;	Gaps 3;
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QY	226	ATGAAAGGAACCTGTGGAAATTTAAAAATGTTCTTCAATATTCATCAAGACCAATCTATC	285	
DB	1586	ATTAAAGGGAATTTGGAATTCAGAAATGTTCACTTCAGTTTACGCATCTCGAAAGAAGTT	1645	
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DB	1646	ARGATCTTGAAGGGCCCTGAACCTGAAGGTGCAGATGGCAGACGGTGGCCCTGGTTTGA	1705	
QY	346	CTCAATGGCAGTGGGAAGAGTACGGTAGTCCAGCTTCTGCAGAGAGTTTATATGATCCGGAT	405	
DB	1706	AACAGTGGCTGTGGGAAGACACAAACAGTCCAGCTGATGCAGAGGCTCTATGACCCACA	1765	
QY	406	GATGGCTTTATCATGTGTGGATGAGATGACATCAGAGCTTTAAATGTGCGGCATTTATCGA	465	
DB	1766	GAGGGGATGGTCAGTGTGTGATGGAACAGGATATTAGGACCAATAATGTAAAGGTTTCTACGG	1825	
QY	466	GACCATATTGGAGTGGTTAGTCAAGAGGCTGTTTTGTTTCGGGACCAACCATCAGTAACAAT	525	
DB	1826	GAAATCAATTGGTGTGGTGTAGTCAGGAACCTGTATTTGTTCCACCAAGTAGCTGAAAC	1885	
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QY	586	AATGCGTATGATTTTATCATGGAGTTTCCTTAATAAAATTAATACATTGGTAGGGGAAAAA	645	
DB	1946	AATGCCATGACTTTATCATGAAACTGCCTCATAAATTTGACACCCCTGGTTGGAGAGAGA	2005	
QY	646	GGAGCTCAAAATGAGTGGAGGCGCAAAACAGAGGATCGCAATTGCTCGTGCTCTAGTTTCGA	705	
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QY	706	AACCCCAAGATTCTGATTTTATGATGAGGCTACGCTCGCCCTGGATTCAGAAAGCAAGTCA	765	

Db	3146	GT	TTCTTTGACTCAGGAGCAGAAGTTTGAACATATGTATGCTCAGAGTTTGCAGGTACCA	3200
Qy	1804	CA	CAGAAATACCTCGAAGAAAGCACAGATTATTTGGAAGCTGTGTATGATTCAGACCCATGCC	1863
Db	3206	TA	CAGAAACTCTTTGAGCAAAAGCACACATCTTTTGGAAATACATTTTCTTCCATCCACGAGCA	3265
Qy	1864	TT	TATATATTTTGCCTATGACAGCAGGGTTCGATTTTGGAGCCTATTTAAATTCAGGCTGGA	1923
Db	3266	AT	GAATGATTTTCTTATGCTGGAATGTTTCCGGTTTGGAGCCTACTTGTGTGGCACATAAA	3325
Qy	1924	CG	AATGACCCAGAGGGCATGTTTCATAGTTTTTTACTGCAATTCATATGAGTATGTGGCC	1983
Db	3326	CT	CATGAGCTTTGAGGATGTTCTGTTAGTATTTTCAGCTGTGTCTTGTGTCATGGCC	3385
Qy	1984	AT	CGAATAAAGCTCGCTTTTGGCTCTCGAATATTCGAAGCCAAATCGGGGCTGGCAT	2043
Db	3386	GT	GGGCAAGTCAGTTCATTTGCTCTCGACTATGCCAAGGCCAAATATCAGCAGGCCAC	3445
Qy	2044	CT	GTTTCCCTTGTGGAAAAAACAACAAATATAGACAGCCGAGTCAGAAAGGAAAAAG	2103
Db	3446	AT	CATCATGATCATTTGAAAAAACCCTTCTGATTTGACAGCTACAGCAGGAGGCTTAATG	3505
Qy	2104	CC	AGACACATGTGGAAGGAAATTAGAGTTTTCGAGAAGTCTCTTTCTTCTATCCATGTCG	2163
Db	3506	CC	GAACACATTTGGAAGGAAATGTCAATTTGGTGAAGTTGTAATCAACTATCCACCCGA	3565
Qy	2164	CC	GATGTTTTTCATCTCTCCGTGCTTATCCCTCAGTATTCAGCGAGGAGACAGTAGCA	2223
Db	3566	CC	GACATCCCAAGTCTTTCAGGACCTGAGCCTCGAGGTGAAGAGGCCAGCCTGGCT	3625
Qy	2224	TT	TGTGGGAGCAGCGCTGTGGGAAAGCACTTCTGTCAACTTTTCGACAGACTTTAT	2283
Db	3626	CT	GTGGGACAGCTGGCTGTGGGAGAGCACAGTGGTCCAGCTCTCTGGAGCGTTTCTAC	3685
Qy	2284	GA	CCCCGTGCAGGACAAAGTCTGTGTTGATGTGTGGATGTCGAAGACAAATTAATGTAC	2343
Db	3686	GA	CCCCTTGGCAGGGAAGTGTCTGTATGGCAAGAAATAAAGCGACTGAATGTTTCAG	3745
Qy	2344	TG	CTCCGTTCCCAAAATAGCAATCTGTTCTCCTCAAGAGCCTGTGCTCTTCAACTGCAGATT	2403
Db	3746	TG	CTCCAGCACACCTGGGCATCGTGTCCCAGAGGCCATCCTGTTGACTGCAGATT	3805
Qy	2404	CT	GTGAGAACATCGCCTATGTGTGACACAGCCGTGTGGTGCCTATGATGAGATCAAGAA	2463
Db	3806	GCT	GAGAACATATGCTATGGAGACAAACAGCCGGGTGGTGTCAACGGAAGATTCGTGAG	3865
Qy	2464	GC	CGAAATGCAGCAATATCCATCTCTTTATTTGAAGTCTCCCTCGAATAACAACACA	2523
Db	3866	GC	AGGAAGAGGCCACATACATGCTCTTCATCGAGTCACTGGCTATTAATATAGCAT	3925
Qy	2524	CA	AGTTGGACTGAAGGAGCACAGCTTTCTGGCGGCCAGAAAACAAGACTAGCTATTGCA	2583
Db	3926	AA	AGTAGGACAAAAGAACTCAGCTCTCTGGTGGCCAGAAAACAAGCATTCGCTAGCT	3985
Qy	2584	AG	GGCTCTTCTCCAAAAACCAAAATTTATTTGTTGATGAGGCGCACTTCGCGCTCGAT	2643
Db	3986	CG	TGCCCTTGTGTAGACAGCCTCAATTTTCTTTTGGTAAGCCAGCTCAGCTCTGGAT	4045
Qy	2644	AA	TACAGTGAAGGTGGTTTCAGCATGCGCTTTCATAAAGCCAGGACGGGAAGCATGC	2703
Db	4046	AC	AGAAATGAAAGGTGTGCCAGAGCCCTGGAACAAGCCAGAGAGGCCCGCACCTGC	4105
Qy	2704	CT	AGTGTGCTACTACAGGCTCTCTGCAATTCAGAAAGCAGATTTGATGTGTTCTGCAAC	2763
Db	4106	ATT	GTGATTTGCTCACCGCCTGTCCACCATCCAGATGSCAGACTTAATAGTGTGTTTCAG	4165
Qy	2764	AA	TGGAAGATTAAGGAACAGGAATCTCATCAAGAGCTCTCTGAGAAATCGAGACATATAT	2823
Db	4166	AA	TGGCAGATCAAGGAGCATGSCACGCAATCAGCACTGCTGTGSCACAGAAGGCATCTAT	4225
Qy	2824	TT	TAAATTTAGTAATGCAAGTACAG	2848
Db	4226	TTTT	CAATGGTCAAGTGTCCAGGTG	4250

RESULT 9

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US-10-072-621-2
; Sequence 2 Application US/10072621
; Publication No. US20020169137A1
; GENERAL INFORMATION:
; APPLICANT: Retner, Peter B.
; APPLICANT: Connop, Bruce P.
; APPLICANT: Pollard, Michelle
; TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
; BY MODIFICATION OF ABC TRANSPORTER EXPRESSION OR ACTIVITY
; FILE REFERENCE: 100103.402
; CURRENT APPLICATION NUMBER: US/10/072,621
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-621-2

```

Query Match	36.1%;	Score 1030.2;	DB 14;	Length 4643;
Best Local Similarity	62.2%;	Pred. No. 4.1e-269;		
Matches 1695;	Conservative 0;	Mismatches 988;	Indels 42;	Gaps 3;
QY	166	ATTATTGATAGAAACCCAGTATAGATTAACCTTTCACACAGCTGGATATAAACCTGAATCC	225	
DB	1523	ATAATTGATATATAGCCAGTATTCACGCTATTCGAAGTGGGCACAAACAGATAAT	1582	
QY	226	ATAGAGGAACCTGTGGAAATTTAAATATGTTCTTCAATATTCATTCAGACCATCTATC	285	
DB	1583	ATTAAGGGAAATTTGGAATTCAGAAATGTTCACTTCAGTTAGCCATCTCGAAAGAAGTT	1642	
QY	286	AGATCTCAGAGGCTCGAATCTCAGAAATTAAGTCTGGAGAGACAGTGCCTTGGTCGT	345	
DB	1643	AGATCTTGAGGGCTCGAACCTGAAGGTGCAGATGGGCAGCGGTGCCTCTGGTTGA	1702	
QY	346	CTCAATGGCAGTGGGAAGTAGTACGGTAGTCCAGCTTCTGCAGAGGTTATATGATCCGAT	405	
DB	1703	AACAGTGGCTGTGGGAAGAGCACAAAGTCCAGCTGATGCAGAGGCTCTATCACCCACA	1762	
QY	406	GATGGCTTTATCATGGTGATAGATATGACATCAGAGCTTTAAATGTGGGCATTATCGA	465	
DB	1763	GAGGGGATGGTCAGTGTTCATGGACAGGATATTAGGACCATTAATGTAAAGGTTCTACGG	1822	
QY	466	GACCATATTGGAGTGGTTAGTCAAGAGCCTGTTTGTTCGGCACCAACCATCAGTAACAAT	525	
DB	1823	GAATCATTTGGTGTGGTGAGTCAGAACTGTATTGTTGCCACCAACGATAGCTGAANAC	1882	
QY	526	ATCAAGATATGACAGATGATATGACTGATGAAGAGATGGAGAGAGCACGAAGGAGCA	585	
DB	1883	ATTGGCTATGGCCGTGAAATGTCCACATGGATGAGATTGAAAGACTCTCAAGGAAGCC	1942	
QY	586	AATGGTATGATTTATCATGAGGTTTCTATTAATTTAATACATTGGTATGGGGAATA	645	
DB	1943	AATGGCTATGACTTTATCATGAACCTGCCTCTAAATTTGACACCTCGTTGGAGAGCA	2002	
QY	646	GGAGCTCAAAATCAGTGGAGGGCAGAAACAGAGGATCGCAATTGCTCGTGCCTTAGTTCGA	705	
DB	2003	GGGGCCCACTTGATGGTGGGCAGAGCAGAGGATCGCCATTGACGTGCCCTGGTTCCG	2062	
QY	706	AACCCCAAGATTCGATTTTAGATGAGGCTAGCTGTGCCCTGGATTCAGAAAGCAAGTCA	765	
DB	2063	AACCCCAAGATCCTCCTGTGATGAGGGCAGCTCAGCCCTTGGACACAGAAAGCGAAGCA	2122	
QY	766	CGTGTTCAGAGTGCATCTGGAGAAGGCGAGCAAAAGGTGCGACTACAACTCGTGGTAGCACAC	825	
DB	2123	GTGGTTTCAGTGTGCTCTGATATAGGCCAGAAAGGTGCGACCACCACTTGATAGTCTCAT	2182	
QY	826	CGACTTTCTACTATTTCGAAGTGCAGATTTGATTTGTGACCCCTAAAGGATGGATGCTGGCG	885	

QY	1924	CGAATGACCCGAGAGGGCAGTGTTCATAGTTTTTATCTGCAATTGCAATTTGGAGCTATGGCC	1983
DB	3323	CTCATGAGCTTTGAGGATGTTCTGTTAGTATATTTTCAGCTGTGTCTTTGGTGGCCATGGCC	3382
QY	1984	ATCGGAAAAACGCTGCTGTTTGGCTCCTCAATATTCGAAAGCCAAATCGGCGGCTCGCAT	2043
DB	3383	GTGGGGCAGTCACTGATTCATTTGCTCTGACTATGCCAAGCCAAATATCAGCACCCAC	3442
QY	2044	CTGTTTGGCTTTGCGAAAAAGAACCAATATATAGACGCGGAGTCAGAGGAGGAAAAAG	2103
DB	3443	ATCATCATGATCAITTTGAAAAAACCCCTTTGATTTGACGTACAGCACGGAAGGCCATAATG	3502
QY	2104	CCAGACACATGTGAAGGGAATTTAGAGTTTCGAGAAGTCTCTTTCTCTATCCATGTCGC	2163
DB	3503	CCGAACACATTCGGAAGGAATGTCAATTTGGTGAAGTTGTATTCAACTATCCACCCGA	3562
QY	2164	CCAGATGTTTTCAATCCTCCGTGGCTTATCCCTCAGTATTGACGCGAGGAAAAAGCATAGCA	2223
DB	3563	CCGGACATCCCAAGTCTTCAGGGACTGAGCCTGGAGGTGAAGAGGCGCAGACGCTGGCT	3622
QY	2224	TTTGTGGGAGCAGCGGCTGTGGGAAAGCACTTCTGTTCACTTCTCGAGAGACTTTAT	2283
DB	3623	CTGTTGGGAGCAGTGGGCTGTGGGAAAGCACATGGTCCAGCTCCTCGAGCGGTTCTAC	3682
QY	2284	GACCCCGTCAGAGCAAGTGTCTGTTGATGTTGGATGCAAAAGAAATTTGAATGTACAG	2343
DB	3683	GACCCCTGGCAGGGGAAGTGTCTGTTGATGSCAAAGAAATAAAGCGACTGAATGTTCAAG	3742
QY	2344	TGGCTCGGTTCCCAATATAGCAATCGTTCTCMAAGACCTGTGCTCTTCAACTCTCGAGACATT	2403
DB	3743	TGGCTCCGAGCACACTCGGCATCGTGTCCAGSAGCCCATCTCTTTTGACTGTCAGCAATT	3802
QY	2404	GCTGAGAACATCGCTATGGTGACAAACAGCCGTGTGGTGCCATTAGATGAGATCAAGAA	2463
DB	3803	GCTGAGAACATTCCTATGGAGACAACAGCCGGTGGTGTACAGGAAGAGATTGTGAGG	3862
QY	2464	GCCGCAATGACAAATATCAATCTTTTATTTGAAGGTCTCCCTGAGAAATACAAACACA	2523
DB	3863	GCAGCAAGGAGGCCCAACATACATGCTTCATCGAGTCACTGCTCTAATAAATATAGCACT	3922
QY	2524	CAAGTTGGATCGAAAGGAGCACAGCTTTCTGGCGCCAGAAACAAGACTAGCTATTGCA	2583
DB	3923	AAAGTAGGAGACAAGAGAACTCGCTCTCTGTGGCCAGAAACAACGCAATTGCCATAGCT	3982
QY	2584	AGGGCTCTTCTCCAAAAACCCAAAAATTTATTTGTTGATGAGGCCACTTCAGCCCTCGAT	2643
DB	3983	CGTGCCCTTTGTAGACAGCTCATATTTTGTCTTTTGGATGAAGCCACGTCAGCTCGGAT	4042
QY	2644	AATGACATGACAGAGTGTGTCAGCATGCCCTTGATTAAGCCAGGACGGAAGGACATGC	2703
DB	4043	ACAGAAAGTGAAGAGTGTCCAGAAGCCCTTGGACAAAGCCAGAGAGGCCGACCTGCG	4102
QY	2704	CTAGTGGTCACTTCACAGGCTCTCTGCAATTCAGAAACGAGATTTGATAGTTGTTCTGCAAC	2763
DB	4103	ATTGTGATTGCTCACCGCTGTCCACCATCCAGAAATGCAGACTTAATAGTGTGTTTCAG	4162
QY	2764	AATGGAAGATTAAGGACACAGGAATCATTAAGAGCTCTTGAGAAATCGAGACATATAT	2823
DB	4163	AATGGCAGAGTCAAGGAGCATGGCCAGCATCAGCAGCTGCTGGCACAGAAAGGCATCTAT	4222
QY	2824	TTTTAAGTTAGTGAATGCACAGTCAAG	2848
DB	4223	TTTTCAATGGTCACTGTGTCAGGCTG	4247

RESULT 10

US-10-097-340-1

; Sequence 1, Application US/10097340

; Publication No. US20030087250A1

; GENERAL INFORMATION:

; APPLICANT: John MONAHAN

; APPLICANT: Manjula GANNAVARAPU

RESULT 10
US-10-097-340-1
; Sequence 1, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GASNAVARAPU

```

/ APPLICANT: Sebastian HOERSCH
/ APPLICANT: Shubhangi KAMATKAR
/ APPLICANT: Steve G. KOVATS
/ APPLICANT: Rachel E. MEYERS
/ APPLICANT: Michael MORRISSEY
/ APPLICANT: Peter OLANDT
/ APPLICANT: Ami SEN
/ APPLICANT: Peter VEIBY
/ APPLICANT: Gordon B. MILLS
/ APPLICANT: Robert C. BAST, Jr.
/ APPLICANT: Karen LU
/ APPLICANT: Rosemarie SCHMANDT
/ APPLICANT: Xumei ZHAO
/ APPLICANT: Karen GLATT
/ TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
/ TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
/ FILE REFERENCE: MEI-030
/ CURRENT APPLICATION NUMBER: US/10/097,340
/ CURRENT FILING DATE: 2002-03-14
/ PRIOR APPLICATION NUMBER: 60/276,025
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/325,149
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 60/276,026
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/324,967
/ PRIOR FILING DATE: 2001/09/26
/ PRIOR APPLICATION NUMBER: 60/311,732
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: 60/325,102
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 60/323,580
/ PRIOR FILING DATE: 2001-09-19
/ NUMBER OF SEQ ID NOS: 363
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 4643
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-097-340-1

Query Match 36.1%; Score 1030.2; DB 15; Length 4643;
Best Local Similarity 62.2%; Pred. No. 4.1e-269;
Matches 1695; Conservative 0; Mismatches 998; Indels 42; Gaps 3;

Qy 166 ATATTGATTAAGAAACCAGGATAGATACTTTCCACAGCTGGATATAAACCTGAATCC 225
Db 1523 ATAATTGATTAATAGCCCAAGTATTGACAGCTATTTCGAAGATGGGCCACAAACCAGATAAT 1582
Qy 226 ATAGAAGAACTGTGGAAATTAATAAATGTTTCTTTCAATTATCCATCAAGACCATCTATC 285
Db 1583 ATTAAGGGAATTTGGAAATTCAGAAATGTTCACTTCAGTTACCATCTCGAAGAAGATT 1642
Qy 286 AAGATTCGAAAGCTCTGAATCTCAGAAATTAAGTCTCGAAGACAGTCGCTTGGTCGGT 345
Db 1643 AAGATCTTGAAGGGTCTGAACTTGAAGTGCAGAGTGGGACAGCGTGGCCCTGGTTGGA 1702
Qy 346 CTCAATGGCAGTGGAGAGTAGGTTAGTCCAGCTTCTCGAGAGGTTTATATGATCCGGAT 405
Db 1703 AACAGTGGCTGTGGGAAGAGCAAAAGTCCAGCTGATGAGAGGCTCTTTGACCCACAA 1762
Qy 406 GATGGCTTTATCATGTTGGTAGAATGACATCAGAGCTTTAAATGTGGGCAATTAFCGA 465
Db 1763 GAGGGGATGCTCAGTGTGTGATGGACAGGATATTAGGACCAATAATGTAAAGTTTCTACGG 1822
Qy 466 GACCATATTCGAGTGGTTAGTCAAGAGCCCTGTTTGTTCGGGACCCACCATCAGTAACAAT 525
Db 1823 GAAATCAATTGGTGTGGTGTGAGTCAGGAACCTGTATTTGTTCGCCACCATGAGTGAANAAC 1882
Qy 526 ATCAAGTATGGAACGAGATGATGTGACTGTATGAGAGAGATGGAGAGAGCAGCAAGGAAAGCA 585
Db 1883 ATTTCGCTATGTCCTGAAATATGTCACCATGATCAGATTCAGAAAGCTGTTCACAGGAAGCC 1942

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Db 3023 ATTGCAATAGCAGAGTTGTTGAATGAAATGTTGCTGGACAGCACTGAAGATAAG 3082
 Qy 1584 CAAGAACTTAAGCATGCTGGAAAGATAGCAACTGAAGCTTTGGAGAAATATACGTACTATA 1743
 Db 3083 AAAGAACTTAGAAGTGTGGGAAGATGCTACTGAAGCAATAGAAAACTTCGGAACCGTT 3142
 Qy 1744 GTGTCAATTAACAGGGAAGAAAGCCCTCGAGCAAAATGATGAAGAGATGCTTCAGACTCAA 1803
 Db 3143 GTTCTTTGACTCAGGAGCAGAGTTTGACATATGATGCTCAGAGTTTGCAGGTACCA 3202
 Qy 1804 CACGAAATACCTCGAAGAAAGCAAGATTAATGGAAGCTGTTATGCAATCAGCCATGCC 1863
 Db 3203 TACAGAACTCTTTGAGGAAGCAACATCTTTTGAATTAATTTCTTCCTTCACCCAGCA 3262
 Qy 1864 TTTATATATTTGCTATGACAGAGGTTTCGATTTGGAGCTTAATTTAAATTCAGCTGGA 1923
 Db 3263 ATGATGATATTTTCTATGCTGGATGTTTCGGTTTGGAGCTACTTTGGTGGACATAAA 3322
 Qy 1924 CGAATGACCCAGAGGGCATGTTTATAGTTTCTTACTGCAATTTGCAATGAGAGCTATGCC 1983
 Db 3323 CTCATGAGCTTTGAGGATGTTCTGTAGTATTTTTCAGCTGTGTGCTTGGTGCATGCC 3382
 Qy 1984 ATCGGAAAGCGCTGTTTGGCTCCTGAATTTCCAAAGCCAAATCGGGGCTGGCAT 2043
 Db 3383 GTGGGCAAGTCAGTTTCAATTTGCTCCTGACTATGCCAAAGCCAAATATCAGCAGGCCAC 3442
 Qy 2044 CTGTTTGCCTTTGTTGAAAGAAACCAATATACAGAGCCGAGTCAAGAGGGAAGAAAG 2103
 Db 3443 ATCATCATGATCATTTGAAAGAAACCCCTTTGATTCAGAGCTACAGCAGGAAGGCTAATG 3502
 Qy 2104 CCAGACATGTGAAGGAATTTAGAGTTTCGAGAGTCTTCTTCTTATCCATGTGCG 2163
 Db 3503 CCGAACATTTGGAAGGAATGTACATTTGGTGGATGTTGATTTCAACTATCCACCCGA 3562
 Qy 2164 CCAGATGTTTTCATCTCCGCTGCTTATCCCTCAGTATTCAGCGAGGAAGACAGTAGCA 2223
 Db 3563 CCGACATCCAGTGTCTCAGGACTGAGCTGAGGTGAGAGGSCCAGACGCTGGCT 3622
 Qy 2224 TTTGTGGGAGCAGCGCTGTGGAAAGACATCTCTGTTTCTTCTGAGAGACTTTAT 2283
 Db 3623 CTGTGGGACAGCTGCTGTGGGAAGACAGTGTCTCAGCTCTCTGGAGCGGTTCTAC 3682
 Qy 2284 GACCCGTCGAGGACAGTCTGTTGATGTTGATGCTGATGCAAGAAATGAATGTACAG 2343
 Db 3683 GACCCCTTGGCAGGGAAGTCTGCTGATGGCAAGAAATGAAGCCACTGMAATGTTACG 3742
 Qy 2344 TGGCTCCGTTCCCAATAGCAATCGTTCTCAGAGCGCTGTCTTCTTCACTGAGCAAT 2403
 Db 3743 TGGCTCCGAGCACACCTGGGCAATCGTGTCCAGAGGCCATCTGTTTGTGACTGAGCAAT 3802
 Qy 2404 GCTGAGACATGCTTATGTTGACACAGCGCTGCTGCTGATAGATGAGATCAGACAAAGAA 2463
 Db 3803 GCTGAGAACATTTGCTATGGAGACACAGCGGCTGTTGTCACAGGAGAGATTGTGAGG 3862
 Qy 2464 GCCGCAATGCGCAAAATATCCTTCTTTTATGGAAGTCTCCTCGAGAAATACACACA 2523
 Db 3863 GCAGCAAGGAGGCCAACATACATGCTTCTATGAGTCACTGCTTAAATATATAGCACT 3922
 Qy 2524 CAAGTTGCACTGAAGGAGCAGCTTTCTGGCGCCAGAAAGCAAGAACTAGCTATGCA 2583
 Db 3923 AAAGTAGAGCAAGGAACCTCAGCTCTCTGGTGGCCAGAAACCAACGCAATGCGCATGCT 3982
 Qy 2584 AGGGCTCTTCTCCAAAGCCCAAAATTTATTTGATGAGGCACTTCAGCCCTCGAT 2643
 Db 3983 CGTGGCTTTGTAGACAGCTCATATTTGCTTTTGGATGAGCCACGTCAGCTCTGGAT 4042
 Qy 2644 AATGACATGAGAGGTGGTTGACATGCCCTTGTATTAAGCCAGGACGGAGAGCATGTC 2703
 Db 4043 ACAGAAAGTGAAGGTTGTCAAGAGAGCCCTGACCAAGAGCCAGAGAGGCGCACCTGC 4102
 Qy 2704 CTAGTGGTCACTCAGAGGCTCTCTGCAATTCAGAAAGCAGATTTGATAGTGGTTCTGCAC 2763

Db 4103 ATTGTGATTGCTCAGCGCTGTCCACATCCAGAAATGCAGACTTATATAGTGGTGTTCAG 4162
 Qy 2764 AATGGAAGATTAAGGAACAGGAAGTCAATCAAGAGCTCTCAGAAATCGAGCATATAT 2823
 Db 4163 AATGCGAGAGTCAAGAGAGATGCGCATCAGCAGCTCTCTGCGACAGAAAGSCATCTAT 4222
 Qy 2824 TTTAAGTTAGTGAATGCACAGTCAG 2848
 Db 4223 TTTCAATGTCAGTGTCCAGGCTG 4247

RESULT 11
 US-10-007-926A-258
 ; Sequence 258, Application US/10007926A
 ; Publication No. US20030143539A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BERTUCCI, FRANCOIS
 ; APPLICANT: HOULCAITE, REMI
 ; APPLICANT: BIRNBAUM, DANIEL
 ; APPLICANT: NGUYEN, CATHERINE
 ; APPLICANT: VIENS, PATRICE
 ; APPLICANT: FERT, VINCENT
 ; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
 ; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
 ; FILE REFERENCE: 1546-R-00
 ; CURRENT APPLICATION NUMBER: US/10/007,926A
 ; PRIOR FILING DATE: 2001-12-07
 ; PRIOR APPLICATION NUMBER: 60/254,090
 ; PRIOR FILING DATE: 2000-12-08
 ; NUMBER OF SEQ ID NOS: 468
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 258
 ; LENGTH: 4643
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: atp-binding cassette, sub-family b
 ; OTHER INFORMATION: (mdr/lep), member 1 (ABCB1) gene.
 US-10-007-926A-258

Query Match 36.1%; Score 1030.2; DB 15; Length 4643;
 Best Local Similarity 62.2%; Pred. No. 4.1e-269;
 Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;

Qy 166 ATTATTGATAAGAAACCCAGATAGATTAATTTCCACAGCTGGATATAAACTGTAATCC 225
 Db 1523 ATATTTGATTAATAGCCAGTATTCAGCTATTTCGAGAGTGGGCAAAACCATATAT 1582
 Qy 226 ATAGAAGGAAGTGGAAATTTAAATGTTCTTTCAATTTATCCATCAAGACCATCTATC 285
 Db 1583 ATTAGGGAAATTTGGAATTCAGAAATGTTCACTTCAGTTACCCATCTCGAAAAAGAGTT 1642
 Qy 286 AAGNTTCTGAAAGTCTGAAATCTCAGATTAAGTCTGGAGACAGAGTGCCTTGGTCGGT 345
 Db 1643 AAGTCTTGAGGGTCTGAACTGAACTGAGGTGCGAGATGGGCAACGGTGGCCCTGTTGGA 1702
 Qy 346 CTCAATGGCAGTGGGAAGATGACGGTAGTCCAGCTTCTGCGAGAGTTATATATCCGGAT 405
 Db 1703 AACAGTGGCTGTGGGAAGAGCAACAGTCCAGCTGATGTCAGAGGCTCTATGACCCACA 1762
 Qy 406 GATGGCTTTATCATGTTGATGAGATGCAATCAGAGCTTTTAAATGTCGGGCAATATCCA 465
 Db 1763 GAGGGGATGGTCAAGTGTGATGAGACAGGATATAGACCATAAATGTAAGGTTTCTACGG 1822
 Qy 466 GACCATATTTGAGTGGTTAGTCAAGAGCTGTTTGTTCGGGACCACTCATCAGTAAACAAT 525
 Db 1823 GAAATCATTTGTTGTTGATGAGTCAAGAACTGTATTTGTTGCCACACGATAGCTGAAAC 1882
 Qy 526 ATCAAGTATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 585
 Db 1883 ATTGCTATGTCGCTGAAAAATGTCACCATGATGATGATGATGATGATGATGATGATGATG 1942
 Qy 586 AATGCGTATGATTTTATCATGAGTGTTCCTAATAAATTTAATACATTTGTTAGGGAAAAA 645

[illegible]

3023	ATTGCAATAGCAGGAGTGTGTGAAATGAAATGTTGTCGACCAAGCACCTGAAAGATAAG	3082
1684	CAAGAACTTAAAGCATGCTGGAAAGATAGCAACTCAAGCTTTGGAGAAATATACGTACTATATA	1743
3083	AAAGAACTTAGAAGTGTGGGAAGATCGCTACTGAAGCAATAGAAAACCTTCCGAACCGTT	3142
1744	GTGTCAATTAAACAGGGAAAAAGCCTTCGACCAATGTAAGAGATGCTTCAGACTCAA	1803
3143	GTTCCTTTTGACTCAGGAGCGAAGTTTGAACATATGTATGCTCAGAGTTTTCAGAGGTACCA	3202
1804	CACAGAAATACCTCGAAGAAAGCACAGATTATTTGGAAGCTGTTATGCAATTCAGCCCATGCC	1863
3203	TACAGAAACTCTTTGAGAAAGCACACATCTTTTGGAAATACATTTTCTTCACCCAGGCA	3262
1864	TTTATATATTTTGCCTATGACAGAGGGTTTCGATTTTGGAGCCTATTTAATTCAGAGCTGGA	1923
3263	ATGATGATATTTTCTATGCTGGAAGTTTCCGGTTTGGAGCCTACTTGGTGGCACATAAA	3322
1924	CGAATGACCCCGAGAGGCATGTTTCATAGTTTTTACTGCAATTCGATATGAGACTATGGCC	1983
3323	CTCATGAGCTTTGAGGATGTCTCTGTAGTATTTTCAGCTGTGTCTTTGTCGCAATGGCC	3382
1984	ATCGGAAAAACGCTGCTGTTTTGGCTTCCTGAAATATTTCAAAGCCAAATCGGGGGCTGGCAT	2043
3383	GTGGGCAAGTCAGTTCAITTTGCTCTCTGACTATGCCCCAAAGCCAAAAATATCAGCAGAGCCAC	3442
2044	CTGTTTCCCTGTTTGGAAAAAGAAACCAATATATAGACAGCGCGAGTCAAGAGGAGGAAAAAG	2103
3443	ATCATCATGATCATTTGAAAAAACCCTTTGATTTGACAGCTACAGCAGGAGAGCCCTAATG	3502
2104	CCAGACACATGTGGAAGGGAATTTAGAGTTTTCGAGAAAGTCTCTTTCTTCTATCCAGTCCG	2163
3503	CCGAAACATTTGGAAGGAAATGTACATTTTGGTGAAGTTGTATTCAACTATATCCACCCGCA	3562
2164	CCAGATGTTTTTCACTCCCTGCTTATCCCTCAGTATTTGAGCGAGAGAAAGACAGTAGCA	2223
3563	CCGACATCCGAGTGTCTTCAGGAGACTGAGCCTCGAGGTGAAGAGGCGCAGACGCTGGCT	3622
2224	TTTGTGGGACGACGGCTGTGGGAAAAAGCACCTCTGTTCAACTTCGACAGACCTTTAT	2283
3623	CTGCTGGGACGACGTGGCTGTGGGAAGACACAGTGTCCAGCTCTCTGGAGCGTTCTAC	3682
2284	GACCCCTGCAAGGACAGTGTCTGTTTGTATGTTGGATGCAAAAGAAATTTGAATGTACAG	2343
3683	GACCCCTGGCAGGGAAGTGTCTGTGATGGCAAAAGAAATAAAGCGACTGAATGTTCAG	3742
2344	TGGCTCGTTTCCAAATAGCAATCGTTCTCAAGAGCCTGTGTCTTTCAACTGCAGCAATT	2403
3743	TGGCTCCGACGACACCTGGGCATCTGTCTCCAGGAGCCCATCTCTTTGACTTCGACATT	3802
2404	GCTGAGAACATCCCTATTGTTGTACACACGCGGTGTGTCCTATTGATGAGATTCAAAGAA	2463
3803	GCTGAGAACATTGCCTATTGAGACAAACAGCCGGTGTGTCTACAGGAAGAGATTGTGAGG	3862
2464	GCGCAATTCGACCAATATCCATTCTTTATTGAAGTCTCCCTGAGAAATACAAACACA	2523
3863	GCGCAAGGAGGCGCAATATCATGTCCTTCATGAGTCACTGCTGCTAATTAATATAGCACT	3922
2524	CAAGTTTGGACTGAAGGAGCACAGCTTTTCGGCGGCCAGAAAAAAGACTAGCTATTGCA	2583
3923	AAAGTAGAGACAAAGGAACTCAGCTCTCTGCTGGTGGCCAGAAAAAAGCGCATTCCTAGCT	3982
2584	AGGCTCTTCTCAAANAACCAAAATTTTATTTGTGGATGAGGCCACTTTCAGCCCTCGAT	2643
3983	CGTGCCCTTGTAGACAGCCCTCATATTTTGTCTTTTGGATGAAGCCACGTCAGCTCTGGAT	4042
2644	AATGACAGTGTGAGAGGTGGTTTCAGCATGCCCCCTTGATTAAGCCAGGACGGGAAGGACATGC	2703
4043	ACAGAAAGTGAAGAAGTGTGCAAGAAGCCCTGGACAAAGCCAGAGAGAGGCCGACCTGC	4102
2704	CTAGTGGTCTCTACAGGCTCTCTCGAATTCAGAACGCGAGATTTGATAGTGGTTCTGCAAC	2763
4103	ATTGTGATGCTCACCGCTGTCCACCATTCAGAAATGTCAGACTTAATATGTTGTTGTTTACG	4162

QY 2764 AATGGAAGATTAAGGACCAAGGAATCATCAAGAGCTCTGAGAAATCGAGACATATAT 2823
 Db 4163 AATGGCAGATCAAGGAGCATGGACGCTCAGAGCTGCTGGCAGAGAGGCTATAT 4222
 QY 2824 TTTAAGTTAGTAATGCACAGTCAG 2848
 Db 4223 TTTTCAATGGTCACTGCTCCAGGCTG 4247

RESULT 12

US-10-641-643-1167
 ; Sequence 1167, Application US/10641643
 ; Publication No. US20040077003A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; Susan G. Stuart
 ; Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/641,643
 ; FILING DATE: 14-Aug-2003
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: <Unknown>
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0001 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1167:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4646 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GENBANK
 ; CLONE: g187468
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1167 :

Query Match 36.1%; Score 1030.2; DB 17; Length 4646;
 Best Local Similarity 62.2%; Pred. No. 4.1e-269;
 Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;
 QY 166 ATATTGTAAGAAACCCAGTATAGATAACTTTTCCACAGCTGGATATAAACTTGAATCC 225
 Db 1526 ATATTGTAATAGCCAAAGTATTGACAGCTATTGGAAGCTGGGCAACAAACAGATAAT 1585
 QY 226 ATAGNAGCACTGGGAAATTAATAATGTTCTTTCATTTATCCATCAAGACCATCTATC 285
 Db 1586 ATTAGGGAAATTTGGAATTCAGAAATGTTCACTTCACTTACCCATCTCGAAAAGAGTT 1645
 QY 286 AAGATTCTGAAGGTCGATCTCAGAATTAAGTCTGGAGAGACAGTCCGCTTGGTGGT 345

Db 1646 AAGATCTTGAAGGGCTGAACCTGAAGGTGCAGAGTGGGCAGACGGTGGCCCTGGTTGA 1705
 QY 346 CTCMAATGSCAGTGGGAAGAGTAGCTAGTCCAGCTTCTGACAGGGTTATATGATCCGGAT 405
 Db 1706 AACAGTGGCTTGGGAAGAGCAACAGCTCAGCTGATGACAGAGGCTCTATGACCCCA 1765
 QY 406 GATGGCTTTATCATGGTGGATCAGAAATGATCATGAGCTTTTAAATGTCGGCATTTATCA 465
 Db 1766 GAGGGGATGGTCACTGTTGATGGACAGGATATTAGACCATAAATGAAGGTTTCTACGG 1825
 QY 466 GACCATATTGGAGTGGTTAGTCAAGAGCCTGTTTCTGGGACCAACCATCAGTACCAAT 525
 Db 1826 GAAATCATTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1885
 QY 526 ATCAAGTATGGACGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 585
 Db 1886 ATTGCTATGGCGGTGAAAATGTCCATGATGATGATGATGATGATGATGATGATGATGATGAT 1945
 QY 586 AATGCTATGATTTATCATGGAGTTTCTTAATAAATTTAATACATTTGATGATGATGATGATGAT 645
 Db 1946 AATGCTATGATTTATCATGAACTGCTCTAATAATTTGACACCTGGTGGAGAGAGA 2005
 QY 646 GAGAGCTCAAAATGATGGAGGCGAGAAACAGAGATCGCAATTCCTGCTGCTGCTGCTGCTGCTG 705
 Db 2006 GGGGCCAGTTGAGTGGTGGGAGAGAGAGATGCGCCATTGACGTGCCCTGGTTGCG 2065
 QY 706 AACCCCAAGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 765
 Db 2066 AACCCCAAGATTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2125
 QY 766 GCTGTTCAAGCTGCACTGAGAGAGGCGAGAAAGGTCGAGCTACAAATCTGCTGCTGCTGCTGCTG 825
 Db 2126 GTGGTTCAAGTGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2185
 QY 826 CGACTTTTCTATTCGAAAGTCAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 885
 Db 2186 CGTTTGTCTACAGTTCTGTAATGCTGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2245
 QY 886 GAGAGAGGAGCAGATGCTGAATTAATGCGCAACAGAGCTCTATATTTTCACTTGTGATG 945
 Db 2246 GAGAAAGGAAATCATGATGAATTAATGAGTTGAAATAGAAATGCGAGCTGATGAATCCAAAGTGAA 2305
 QY 946 TCAAGGATATTTAAAAAGCTGATGAACAGATGAGTCAATGACATATTTCTA----- 997
 Db 2306 ATGCAGACAGCAGGAAATGAAGTTGAAATAGAAATGCGAGCTGATGAATCCAAAGTGAA 2365
 QY 998 -----CTGAAAGAAAGACCAACTCTCTCTGCACTCTCTGCAAGAGCATCA--- 1045
 Db 2366 ATTGATGCTTGGAAATGCTTCAAAATGATTCAGATCCAGTCTAATAAGAAAAAGATCA 2425
 QY 1046 -----AGTCAGACTTCAITTCAGAGGCTGAGGAATCCACCCCAATCT 1086
 Db 2426 ACTCGTAGGAGTGTCCGTGGATCACAAGCCCAAGACAGAAAGCTTAGTACCAAGAGGCT 2485
 QY 1087 AAAGAGATAGTCTTCTGAGTCTCTCTATTAATAATTTTAAAGTTAAACAGCTGAA 1146
 Db 2486 CTGGATGAAGATATACCTCCAGTTTCTTTTGGAGGATTTATGAAGCTAAATTTAACTGAA 2545
 QY 1147 TGGCTTTTGTGGTCTGGGGCAATTTGGCTTCTTTCTAAATGGAATCTGTTCAATCCAGTA 1206
 Db 2546 TGGCTTTATTTTGTGGTGTATTTTGTGCAATTTAATATGAGGCTCTGCAACCCAGCA 2605
 QY 1207 TTTTCCATCATCTTGGCAAAATTAACCACTGTTGGAAATTAATGATTAACCAATTA 1266
 Db 2606 TTTGCAATAATAATTTTCAAGATTTATAGGGGTTTTCACAGAAATGATGATGATGATGATGATGAT 2665
 QY 1267 AAG---CATGATGCAGAAATTTATTCATGATATTCGTCAATTTGGTGTGTTATTTGCTTT 1323
 Db 2666 AAAGCAGATAGTAACTTGTGTTTCACTATTTGTTTCTAGCCCTTGGAAATTTATTTCTTT 2725
 QY 1324 GTGATTTATTCAGGAGGATTTATTTACGGCAGAGAGGGAATTTTAAAGATGAGA 1383
 Db 2726 ATTACATTTTCTCAGGGTTTCAATTTGGCAAGCTGGAGATCTCTCACAAGCGG 2785

QY 1384 TTAAGACACTTGGCTTCAAGGCAATGTTATATCAAGATATCCCTGGTTTGATGAAAG 1443
DB 2786 CTCGATACATGCTTTCCGATCCATGCTCAGACAGGATGAGTTGGTTTGATGACCT 2845
QY 1444 GAAACAGCAGCAGGCTTGAACAAATATAGCCATATATAGCAAAATCAAGGA 1503
DB 2846 AAAAAACCACTGAGCAATTTGACTACCGCTCGCAATGCTCTCAAGTTAAGGG 2905
QY 1504 GCAACAGGTTCCAGGATGCGCTTTAAACAACAAATGCAACTAACATGGGACTTTTCAGTT 1563
DB 2906 GCTATAGTTCCAGGCTTGGTAAATTAACCAATATATGCAAAATCTTGGGACAGGAATA 2965
QY 1564 ATCAATTCCTTTATATAGATGGGATGACATTCCTGATCTGATATGCTCCAGTA 1623
DB 2966 ATTATATCCCTTCTATGTTGGCACTAACTGTTACTCTTAGCAATTTGACCCATC 3025
QY 1624 CTTGCCCTGACAGGAATGATTGAAACCGCAGCAATGACTGGAATTTGCAACAAAGATAAG 1683
DB 3026 ATTGCAATAGCAGGATTTGTAATGAATGATGTTGCTGACAGCACTGAAAGATAAG 3085
QY 1684 CAGAACTTAAGCATGCTGAAAGATAGCAACTGAGCTTTGAGAAATATACGTACTATA 1743
DB 3086 AAGAACTAGAGGTGCTGGAGATGCTACTGAGCAATAGAAACTTTCCGAACCGTT 3145
QY 1744 GTGTCATTAAACAGGGAAGGCTTCGAGCAATGATGAAGATGCTTCAGACTCA 1803
DB 3146 GTTCTTTGACTCAGGAGCAGAGTTTGAACATATGATGCTCAGAGTTTGCAGGTACCA 3205
QY 1804 CACAAATACCTCGAAGAAAGCAGATTTATGGAAGCTGTTATGCAATTCAGCCATGCC 1863
DB 3206 TACAGAACTCTTTGAGGAAGCAGACATCTTTGGAATTACATTTCTTCAOCCAGGCA 3265
QY 1864 TTTATATATTTGCTATGAGCAGGCTTTGATTTGCGCCCTATTTAAATCAAGCTGGA 1923
DB 3266 ATGATGATTTTCTTATGCTGATGTTTCCGGTTTGGAGCTACTTTGGTGGCAGATAAA 3325
QY 1924 CGAATGACCCAGAGGCGATGTTTCAATGTTTACTGCAATTTGATGAGCTATGGCC 1983
DB 3326 CTCATGAGCTTTGAGGATGTTCTGTAGTATTTTCACTGTTGCTTTGGTGCCATGCC 3385
QY 1984 ATCGGAAAGCGCTGTTTGGCTCTGATATTTTCAAGGCAATCGGGGCTGGCAT 2043
DB 3386 GTGGGGCAAGTCAGTTCACTTGTCTGCTGACTATGCCAAGCCAAATATCAGCAGGCCAC 3445
QY 2044 CTGTTTGGCTTTGGAAGAAACCAATATACAGCGCGCTCAAGAGGGAAGAAAG 2103
DB 3446 ATCATATGATCATTTGAAACACCCCTTTGATTCAGAGCTACAGCAGGAGGCTTAATG 3505
QY 2104 CCAGACATGTAAGGGAATTTAGAGTTTGAGAGTCTCTTTCTTCTATPCCATGCGC 2163
DB 3506 CCGAACATTTGGAAGGAATGTACATTTTGGTGAAGTTGTTTCAACTATCCACCCGA 3565
QY 2164 CCAGATGTTTTCATCTCCGTGGCTTATCCCTCAGTATTTGAGCGGAGGAAGCAGTAGCA 2223
DB 3566 CCGACATCCAGTCTTTTCAAGGACTGAGCTTGGAGGTGAGAGGGCCAGCCTGGCT 3625
QY 2224 TTTGTGGGAGCAGCGCTGTGGGAAAGCACTTTCTGTTCAACTTTCTGAGAGACTTTAT 2283
DB 3626 CTGTTGGGSCAGAGTGCTGTGGGAAGAGCAGTGTGCTGAGCTCTCTGGAGCGGTTCTAC 3685
QY 2284 GACCCGTCGAGGCAAGTCTGTTTGTGCTGAGTGAAGCAAGATTTCAATGTTACAG 2343
DB 3686 GACCCCTTGGCAGGGAAGTCTGCTGTTGATGGCAAGAAATAAAGCGCACTGAAATGTTTACAG 3745
QY 2344 TGGTCTCCCTTCCCAATAGCAATCGTTCTTCAAGAGCGCTGTGCTCTTCACTGAGCAATT 2403
DB 3746 TGGCTCCGAGCAGACCTCGGCATCGTGTCCAGGAGGCCATCTGTTTGTGCTGAGCATT 3805
QY 2404 GCTGAGAACTGCTCTATGTTGAACAGCCGTTGTGTCCTATTTAGATGATCAAGAA 2463
DB 3806 GCTGAGAACTGCTCTATGTTGAACAGCCGTTGTGTCACAGGAGAGATCGTGAGG 3865

QY 2464 GCCGAAATGACGAAATATCCATCTTTTATTAGAGTCTCCCTCAGAAATACACACA 2523
DB 3866 GCAGCAAGGAGGCGCAACATACATACCTCTCATCGAGTCACTCCCTTAATAATATAGCAT 3925
QY 2524 CAAATTTGAGCTGAAAGGAGCAGCTTTCTGCGCGCCAGAAACAAAGACTAGCTATTGCA 2583
DB 3926 AAGTAGAGAGCAAGGAACTCAGCTCTCTGCTGCGCCAGAAACAAAGCAATGCCATAGCT 3985
QY 2584 AGGCTCTTCTCCAAAAACCCAAATTTTATTGTTGGATGAGCCACTTCAGCCCTCGAT 2643
DB 3986 CGTGCCCTTTTATAGACAGCTCATATTTTGTCTTTTGGATGAGCCAGCTCAGCTCTGGAT 4045
QY 2644 AATGACAGTGAAGAGTGTGTTCCAGATGCCCTTGAATAAGCCAGGACCGGAAAGGACATGC 2703
DB 4046 ACAGAAATGAAAGGTTGTCCAGAGCCCTTGGACNAAGCCAGAGAGAGGCCGACCTGC 4105
QY 2704 CTAGTGTCTCAGCAGAGCTCTCTGCAATTCAGACAGCAGATTTGATAGTGTCTGAC 2763
DB 4106 ATTGTGATTTGCTCAGCGCTGTCCACCATCCAGAAATGCAGACTTAATAGTGTGTTTCAG 4165
QY 2764 AATGAAAGATAAAGAAACAAAGAACTCATCAAGAGCTCTCGAATAATCGACATATAT 2823
DB 4166 AATGCGAGTCAAGAGCATGTCAGCATGATCAGCAGCTCTGCGCACAGAAAGCATCTAT 4225
QY 2824 TTTAAGTTAGTGAATGCACAGTCAG 2848
DB 4226 TTTTCAATGTCAGTGTCCAGGCTG 4250

RESULT 13
US-10-343-657-1
; Sequence 1, Application US/10343657
; Publication No. US20040086882A1
; GENERAL INFORMATION:
; APPLICANT: Roninson, Igor B.
; APPLICANT: Ruth, Adam
; TITLE OF INVENTION: Mutations of the MDR1 P-glycoprotein that improve its
; TITLE OF INVENTION: Ability to Confer Resistance to Chemotherapeutic Drugs
; FILE REFERENCE: 00,616-A
; CURRENT APPLICATION NUMBER: US/10/343,657
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/222,313
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4646
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (425) ..(4264)
US-10-343-657-1

Query Match 36.1%; Score 1030.2; DB 17; Length 4646;
Best Local Similarity 62.2%; Pred. No. 4.1e-269;
Matches 1695; Conservative 0; Mismatches 988; Indels 42; Gaps 3;

QY 166 ATTAATTGATAAGAAACCCAGTATAGATAAATTTTCCAGAGCTGGATATAAACCCTGATCC 225
DB 1526 ATAAATTGATAAATAAGCCAGTATTGACAGCTATTTCGAAGAGTGGGCACAAACAGATAAT 1585
QY 226 ATGAGAGGAGCTGTGGAATTTAAATTTTCTTCAATTTATCCATCAAGACCATCTATC 285
DB 1586 ATTAAGGGAATTTGGAATTCAGAAATTTTCACTTCAGTTACCATCTCGAAAAGAGTT 1645
QY 286 AAGATCTGAAAGCTCTGAATCTCAGAAATTAAGTCTGGAGAGACAGTCCGCTTGGTCGT 345
DB 1646 AAGATCTTGAAGGCTGAACTGAAAGTGCAGAGTGGGCGAGAGCGGCTGGTGGGA 1705
QY 346 CTCAATGGCAGTGGGAAGAGTACGTTAGTCCAGCTTCTCGAGAGGTTATATGATCCGGAT 405
DB 1706 ARCAGTGGCTGTGGGAAGAGCAACAGATCCAGTGTGTCAGAGGCTCTATGATCCCA 1765

QY 406 GATGCTTTATCATGTTGATGAGATGACATCAGAGCTTTAAATGTGCGGATTTATGCA 465
Db 1766 GAGGGATGGTTCAGTGTGATGACAGGATATTAGGACATAAATGTAAAGTTTCTAGCG 1825
QY 466 GACCATATGGAGTGGTGTAGTCAAGAGCTGTTTGTGGGACACCATCAGTAACAAAT 525
Db 1826 GAAATCATGGTGTGGTGTAGTCAAGAACCTGTATGTTTGGCCACCACCATAGCTGAAAC 1885
QY 526 ATCAAGATATGACGAGATGATGTGACTGATGAAGAGATGGAGAGCAGCAAGGAGCA 585
Db 1886 ATTGCTATGGCCGTGAAATGTCACATGGATGAGATTGAAAGCTGTCAAGGAGCC 1945
QY 586 AATGGTATGATTTATCATGAGATTTCTATTAATTAATTAATTAATTAATTAATTAAT 645
Db 1946 AATGGCTATGATTTATCATGAACTGTGCTCAATAATTTGACACCTGTGTGGAGAGA 2005
QY 646 GGAGCTCAAAATGAGTGGAGGAGGAGGAGGAGGATGCAATTTGCTGCTTCTAGTTCGA 705
Db 2006 GGGGCCCATGAGTGGTGGGAGAGCAGAGATCGCATTTGACAGTGGCTGTGCTGCG 2065
QY 706 AACCCCAAGATTCGATTTTATGATGAGGCTAGCTGTGCTGCTGATTCAGAAAGCAAGTCA 765
Db 2066 AACCCCAAGATTCGCTGCTGATGAGGCGCAGCTGAGCTTGGACACAGAAAGCGAAGCA 2125
QY 766 GCTGTTCAAGCTGCACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 825
Db 2126 GTGGTTCAGTGGCTCTGATTAAGCCAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2185
QY 826 CGATTTCTACTATTCGAATGCGAGTTTGTATGAGCCCTAAAGAGTGAATGCTGGCG 885
Db 2186 CGTTTCTACATGCTGTAATGCTGACGTCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2245
QY 886 GAGAGAGGAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 945
Db 2246 GAGAAAGGAAATCATGATGAATGATGAATGATGAATGATGAATGATGAATGATGAATGAT 2305
QY 946 TCACAGGATATTAATAAGCTGATGAACAGATGGAGTCAATGACATATTTCTA ----- 997
Db 2306 ATCCAGACAGCAGGAAATGAAGTTGAATTAGAAATGACAGTGTGATGATGATGATGATGAA 2365
QY 998 -----CTGAAGAAAGACCACTCACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1045
Db 2366 ATTGATGCTTGGAAATGCTTCAATGATTTCAAGATTCAGTCTAATAGAAAGAAAGATCA 2425
QY 1046 -----AGTCAGACTTCATTGACAGGCTGAGGAAATCCCACTT 1086
Db 2426 ACTGTTAGAGTGTCTGATGATCAAGCCAGACAGAAAGCTTAGTACCAAGAGGCT 2485
QY 1087 AAGAGATAGTCTCTGAGGCTCTCTAATTAATAATTTAAAGTTAAAGCTGAA 1146
Db 2486 CTGGATGAAGTATACCTCCAGTTTCTTTTGGAGGATTTATGAAGCTAAATTTAACTGAA 2545
QY 1147 TGCCCTTTGCTGCTGCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
Db 2546 TGCCCTTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2605
QY 1207 TTTTCATCATCTTTGCAAAATTTAATCAATGTTTGGAAATTAATGATTAATTAATTAATTAAT 1266
Db 2606 TTTGCAATAATATTTCAAGATTTATAGGGTTTATCAAGAAATGATGATGATGATGATGATGATGAT 2665
QY 1267 AAG---CATGATGCAAAATTTATCCATGATATTCGCTATTTGGGCTGTTATTTGCTTT 1323
Db 2666 AAGGACAGATAGTACTGTTTTCATATGTTTCTAGCCCTTGGAAATTTATTTCTTTT 2725
QY 1324 GTCAGTATTTCAAGGAGATTTATTTAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1383
Db 2726 ATTACATTTTCTCAGGGTTTCAATTTGGCAAGCTGGAGAGATCTCCCAAGCGG 2785
QY 1384 TTAAGACATGCGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1443
Db 2786 CTCGATACATGTTTTCGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2845

QY 1444 GAAAAAGGACAGAGGCTTTGACAAACATATTATGACCATATAGCACAAATTTCAAGGA 1503
Db 2846 AAAAAACCACTGGAGCATTTGACTACAGGCTGCCAATGATGCTGCTCAAGTTAAAGGG 2905
QY 1504 GCAACAGTTTCCAGGATTTGGCTTTAAACAAAAATGCAAACTAAACATGGGACTTTCAAGTT 1563
Db 2906 GCTATAGTTTCCAGGCTTGTCTTAATTTACCAGAAATATAGCAAACTTTGGGACAGGAATA 2965
QY 1564 ATCATTTCTTTATATATGATGAGGAGATGACATTTCTGATTTCTGAGTATTTGCTCCAGTA 1623
Db 2966 ATTATATCTTTCTATCTATGTTGGCACTAACTGATTTCTTTAGCAATTTGATACCATC 3025
QY 1624 CTTGCGGTGACAGGAATGATTGAAACCGCAGCAATGACTGGAATTTGCAACAAAGATAAG 1683
Db 3026 ATTGCAATAGCAGGATTTGTTGAAATGAAATGTTGTTCTGGAACAAGCACTGAAAGATAAG 3085
QY 1684 CAAGAACTTAAGCATGCTGGAAAGATAGCAACTGAGCTTTGGAGATATACGTACTATA 1743
Db 3086 AAAGAACTAGAGGCTGTGGGAAGATGCTACTGAGCAATAGAAAACTTTCCGAACCGTT 3145
QY 1744 GTGTCATTAAACAGGGAAGAAAGCCCTTCAGCAAAATGATGAAGAGATGCTTTCAAGCTCAA 1803
Db 3146 GTTCTTTGACTCAGGAGCAGAGTTTGAACATATGATGCTCAGAGTTTGCAGGTACCA 3205
QY 1804 CACAGAAATACCTCGAAAGAAAGACAGATTTTGGAAAGCTGTTATGCAATTCAGGCAATGCC 1863
Db 3206 TACAGAAACTCTTTGAGGAAGACACATCTTTGGAATTAACATTTCTTCCACCCAGCA 3265
QY 1864 TTTATATTTTGGCTATGACAGAGGTTTCGATTTGGAGCTATTTAAATTTCAAGCTGGA 1923
Db 3266 ATGATGATTTTCTTATGCTGATGTTTCGTTTGGAGCTTACTTTGGTGGCACAATAA 3325
QY 1924 CGAATGACCCAGAGGCGATGTTTCTATGTTTACTGCAATTTGCAATTTGCAATTTGAGCTATGGCC 1983
Db 3326 CTGATGAGCTTTGAGGATGTTCTGTTAGTATTTTCAGCTGTTGCTTTGTTGCTGCTGCTGCTGCT 3385
QY 1984 ATCGAAATAACGCTGCTTTTGGCTCTGAAATATTCGAAGCCAAATCGGGGCTGCGCAT 2043
Db 3386 GTGGGCAAGTCAAGTTCAATTTGCTCTGACTATGCCAAGCCAAAATATCAGCAGCCAC 3445
QY 2044 CTGTTTGGCTTTTGGAAAAAGAAACCAATATAGACAGCCGAGCTCAAGAGGGAAGAAAG 2103
Db 3446 ATCATCATGATCATTTGAAAGAAACCCCTTTGATTTGACAGCTACAGCAGGAGGCTTAATG 3505
QY 2104 CCAGACATGTTGAAGGAATTTAGAGTTTGGAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2163
Db 3506 CCGAACATTTGGAAGGAATTTGTCATTTTGGTGAAGTTGTTCACTTTGTTCACTATTTCCACCCGA 3565
QY 2164 CCAGATGTTTTCATCTCCGCTGCTTATCCCTCAGTATTCAGCGAGGAAAGACAGTAGCA 2223
Db 3566 CCGACATCCAGTCTTCTGAGGACTGAGCTGAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 3625
QY 2224 TTTGGGGAGCAGCGCTGTGGAAAGACACTTCTGTTCACTTTCTGAGAGACTTTAT 2283
Db 3626 CTGGTGGGACAGCTGCTGTGGGAAGACAGTGGTCCAGCTCTGAGCGGTTCTAC 3685
QY 2284 GACCCGTCAGAGACAGTCTGTTGATGCTGATGCAAAAGAAATTTGAATGTTACAG 2343
Db 3686 GACCCCTTGGCAGGAAAGTCTGCTTGAATGGCAAGAAATTAAGCGCTGATGTTTCAAG 3745
QY 2344 TGGCTCTCCCTCCCAATAGCAATCGTTCTTCAAGAGCTGTGCTTCTCACTCAGGAGCTTT 2403
Db 3746 TGGCTCCGACACACCTGGGCTGCTGCTCCAGGAGGCCATCTCTGTTTGAATCTGAGCAAT 3805
QY 2404 GCTGGAACATGCTGCTATGTTGACAGCGCTGTGGTGGCTATGATGATGATGATGATGATGATGAT 2463
Db 3806 GCTGAGAACATTTGCTATGGAGACAGACCGCGGTGTTGTTGAGGAGAGATCTGTGAGG 3865
QY 2464 GCGCAATGTCAGCAAAATATCCATTTCTTTTATGAGGCTCTCCCTGAGAAATACAACACA 2523
Db 3866 GCAGCAAGGAGGCCAACATACATGCTTCTCATGAGTCACTGCTCTAATAATATAGCACT 3925
QY 2524 CAAGTTGAGTGAAGAGGAGCAGCTTTCTTCTGCGGCGCAGAAACAAAGACTAGCTATTGCA 2583

Db 3926 AAAGTAGGAGACAAAGGAACCTAGCTCTCTGTGGCCAGAAACACGCAATTCGCTAGCT 3985
Qy 2584 AGGGCTTTCTCCAAAAACCCAAAAATTTTATTTGTTGGATGAGGCGCACTTCAGCCCTCGAT 2643
Db 3986 CGTGCCCTTTGTAGACAGGCTCATATTTTGTCTTTGGATGAAGCCACGTCAGCTCTGGAT 4045
Qy 2644 AATGACAGTGAGAGGTGTTTCAAGATGCTTGTATTAAGCCAGGACGCGGAAGGACATGC 2703
Db 4046 ACAGAAAGTGAAAGGTTTGTCAAGAAAGCCCTGGACAAAGCCAGAGAGCGCGACCTGC 4105
Qy 2704 CTAGTGGTCACTCACAGGCTCTCTGCAATTCAGAACCGCAGATTTGATAGTGGTTCTGAC 2763
Db 4106 ATTGTGATTGCTCACCGCTGCTCCACCATCCAGATCCAGACTTAATAGTGGTTTCAG 4165
Qy 2764 AATGGAAGATTAAGAAACAAAGGAACCTCAAGAGCTCTGAGAGCTCTGAGAAATCGAGACATAT 2823
Db 4166 AATGCGAGAGTCAAGGAGCATGCGCATCAGCAGCTGCTGCGACAGAAAGGACATCTAT 4225
Qy 2824 TTTAAGTTAGTGAATGCAGAGTCAG 2848
Db 4226 TTTTCAATGGTCAAGTGTCCAGGCTG 4250

RESULT 14
US-09-866-866A-1
; Sequence 1, Application US/09866866A
; Patent No. US2002010224A1
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Schuetz, John
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
; FILE REFERENCES: 1340-1-021CIP2
; CURRENT APPLICATION NUMBER: US/09/866,866A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/584,586
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: PCT/US99/11825
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/086,988
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-866A-1

Query Match 36.08; Score 1028.6; DB 9; Length 3860;
Best Local Similarity 62.24; Pred. No. 9.8e-289;
Matches 1694; Conservative 0; Mismatches 989; Indels 42; Gaps 3;

Qy 166 ATTATTGATAAGAAACCCAGTATAGATAAAGCTTTCCACAGCTGGATATAAACCCTGAATCC 225
Db 1102 ATAAATTGATTAATGAACCAAGTATTGACAGCTATTGAGAGAGTGGGACAAACAGATAAT 1161
Qy 226 ATGAGGAAGTGTGGAAATTTAAATTTTCTTTTCAATTTATCCATCAAGACCAATCTATC 285
Db 1162 ATTAAGGGAATTTGGAATTCAGAAATGTTCACTTCAGTTTACCCTATCTCGAAAGAAGTT 1221
Qy 286 AAGATTCTGAAAGTCTGAATCTCAGAAATTAAGTCTGACAGACAGTGGCTTTGGTCGGT 345
Db 1222 AAGATCTTGAAGGCTTGAACCTGAAGTTCAGAGTGGGCGAGGCGGCTGGTTGGA 1281
Qy 346 CTCAATGGCAGTGGGAAGAGTACGGTATTCAGCTTCTGACAGAGGTTATATGATTCGGAT 405
Db 1282 AAGAGTGGCTGTGGGAAGAGACAAACAGTCCAGCTGATGACAGAGGCTCTATGACCCCA 1341
Qy 406 GATGGCTTTATCATGGTGGATGAGATGACATCAGAGCTTTTAAATGTGGCGCAATATCGA 465
Db 1342 GAGGGGATGGTCAAGTGTGATGGAGCAGATATTAGGCCAATTAATGTAAGGTTTCTACGG 1401

Qy 466 GACCATAATTGAGTGGTTAGTCAAGAGCCTGTTTGTTCGGGACCCACCATCAGTAACAAT 525
Db 1402 GAATATCATTTGTTGTTGTTGAGTCAGTCAAGAACCTGTATTTGTTGCCACCATAGCTGAAAC 1461
Qy 526 ATCAAGTATGACAGAGATGATGTGATGAAGAGATGAGAGAGCAGCAGAGGGAAGCA 585
Db 1462 ATTGCTATGCGCCGTGAAATGTCCATGATGAGATTGAGAAAGCTGTCAAAGGAAGCC 1521
Qy 586 AATGCTATGATTTTNTCATCGAGTTTCTTAATAAATTTAATACTTGGTAGGGGAAAAA 645
Db 1522 AATGCTATGATTTTATCATGAATCTGCTCATTAATTTGACACCTGTTGGAGAGAGA 1581
Qy 646 GGAGCTCAAAATGAGTGGAGGCGCAGAAACAGAGGATGCGCAANTTGTGCTGCTTGTTCGA 705
Db 1582 GGGGCCCAAGTTGAGTGGTGGGCGCAGAAAGCAGAGGATGCGCAATTCGACGTGCTGTTGCG 1641
Qy 706 AACCCCAAGATTTCTGATTTTATGAGTGGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 765
Db 1642 AACCCCAAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1701
Qy 766 GCTGTTCAAGCTGCACCTGGAGAAAGCGCAGAGGCTCGGACTTACAAATCGTGTAGCACAC 825
Db 1702 GTGGTTCAAGTGGCTCTCGATTAAGGCCAGAAAGGTCGGACCCACCATTTGTATAGTCTCAT 1761
Qy 826 CGACTTTCTATTTGGAAGTGCAGATTTGATTTGACCCCTAAAGGATGGAATGCTGGCG 885
Db 1762 CGTTTGTCTACAGTTCTGTAATGCTGACGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1821
Qy 886 GAGAAAGCAGACATGCTGAACTAATGCAAAACGAGGTCTATATTTTCACTTGTGATG 945
Db 1822 GAGAAGGAAATCATGATGAACTCATGAAGAGAAAGGCAATTTACTTCAAACTTGTGACA 1881
Qy 946 TCACAGGATATTAAAAAGCTGATGAACAGATGGAGTCAATGACATATTTCTA----- 997
Db 1882 ATGCAGACAGCAGAGGAATGAAGTTGAAATTTAGAAAAATGCAGCTGATGAATTCAAAAAGTGA 1941
Qy 998 -----CTGAAAGAAAGAACCAACTCACTTCTCTGCTCTCTGCTCTCTGAGAGCATCA--- 1045
Db 1942 ATTGATGCTTGGAAATGCTTCAATGATTCAGATCCAGTCTAATTAAGAAAGAGATCA 2001
Qy 1046 -----AGTCACACTTCATGACAAAGCTGAGAGGATGAGAGATTCACCAATCT 1086
Db 2002 ACTCGTAGGAGTGTCCGTGGATCAAGGCCCAAGACAGAAAGCTTTAGTACCAAGAGGCT 2061
Qy 1087 AAAGAGATGATGCTTCTGAGTCTCTATTAATAAATTTTAAAGTTTAAACAGGCTGAA 1146
Db 2062 CTGGATGAAGATATACCTCCAGTTCTCTTTTGGAGGATTTAGAGCTTAATTTTAACTGAA 2121
Qy 1147 TGGCCTTTTGTGCTTCTGGGACATTTGCTTCTTAATGGAACCTGTTTCAATCCAGTA 1206
Db 2122 TGGCCTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2181
Qy 1207 TTTTCCATCATCTTTGCAAAAAATTAACCATGTTTGGAAATTAATGATAAAACCAATTA 1266
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Qy 1267 AAG---CATGATGCAAGAAATTTATTTCCATGATTTCTGCTCATTTTGGGTTGTTTGTCTTT 1323
Db 2242 AAAGCAGAAATGATTAATTTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTT 2301
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Qy 1384 TTAAGACATCTGCTTCAAGGCTTCAATTTATATATATATATATATATATATATATATATATATATAT 1443
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 Db 2542 ATATATCTCTTATCTATGATGGTGGCAACTTAACTCTGTACTCTTAGCAATTTGACCCATC 2601
 Qy 1624 CTTCGCGTGACAGCAATGATTAAGAAACCGCAGCAATGACTGCAATTTGCCAAACAAAGATAAG 1683
 Db 2602 ATTGCAATAGCAGGAGTTTGTGNAATGAATGTTGTCTGGACAGCACTGAAGATATAG 2661
 Qy 1684 CAAGAACTTAGCACTGCTGGAAAGATAGCACTGAACTTTGAGCAATATACCTATATA 1743
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 Qy 1744 GTGTCAATTAACAAGGGAAGAAAGCCTTCGAGCAATATGATCAAGAGATGCTTCAGACTCAA 1803
 Db 2722 GTTCTTTGACTCAGGAGCAGAAAGTTTGACAAATGATGATCTCAGAGTTTGCAGGTATCCA 2781
 Qy 1804 CACGAATACCTCGAAGAAAGCAACAGATTAATGGAAGCTGTTATGCAATTCAGCCATGCC 1863
 Db 2782 TACAGAACTCTTTGAGAAAGCAACATCTTTGGAATATACATTTCTTCAACCCAGGCA 2841
 Qy 1864 TTATATATTTTGGCTATGACAGGAGGTTTCGATTTGGAGCTTATTAATTCAGCTGGA 1923
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 Qy 1924 CGAATGCCAGAGGAGCACTTCTATAGTTTCTTACTGCAATTCATATGAGCTATGGCC 1983
 Db 2902 CTCATGAGCTTTGAGGAGTGTCTGTATGATTTTTCAGCTGTTGTCTTGTGGCCTATGCC 2961
 Qy 1984 ATCGAAAGAAAGCTGCTTTGGCTCTGGAATATTTCCAAAGCCAAATCGGGGCTGCCAT 2043
 Db 2962 GTGGGCAAGTCAGTTCAATTTGCTCTGACTATGATGCAAGGCAATATATCAGCAGCCAC 3021
 Qy 2044 CTGTTGCTTGTGGAAGAAAGCAACAAATATAGACAGCGCGCTCAAGAAAGGAAAG 2103
 Db 3022 ATCATCATGATCATGTAAGAAAGACCCCTTGTGATGACAGCTTACAGCAGGAGGCAATATG 3081
 Qy 2104 CCAGACATGTAAGGGAATTTAGAGTTTCGAGAACTCTCTTTCTTATCCATGCTCC 2163
 Db 3082 CCGAACACATTTGAAGGAATGTCACATTTGGTGAAGTTGTATTTCAATCTCCACCCGA 3141
 Qy 2164 CCAGATGTTTTCATCTCCGTTGCTTATCCCTCAGTATTTAGCGGAGAAAGACAGTAGCA 2223
 Db 3142 CCGACATCCCATGCTTTCAGGAGCTGAGCTTGGAGGAGGAGGCGGAGAGCTGCTGCT 3201
 Qy 2224 TTTGTGGGAGCAGCGCTGTGGGAAAGCACTTCTTGTTCAGCTTCTGAGAGACTTTAT 2283
 Db 3202 CTGTTGGGAGCAGCTGCTGTGGGAGAGCACAGTGTCTCCAGCTCTGAGCGGTTCTAC 3261
 Qy 2284 GACCCGCTGCAAGACAGTGTCTGATGTTGATGCTGATGCAAGAAATGATGATGACAG 2343
 Db 3262 GACCCCTTGGCAGGGAAGTGTCTGTTGATGGAAGAAATTAAGCGCACTGGAATGTTGAG 3321
 Qy 2344 TGGCTCCGTTCCCAATAGCAATCGTTCTCAGAGGCTGTGCTCTTCACTGCGAGCAAT 2403
 Db 3322 TGGCTCCGAGCACACCTGGGCATCGTGTCCAGGAGGCCATCTCTTGTGACTGCGAGAT 3381
 Qy 2404 GCTGAGAACTCCGCTATGCTGCAACAGCGGTGTGCTGCTGCTATGATGAGATCAAGAA 2463
 Db 3382 GCTGAGAACTCCGCTATGAGAACACAGCGGCTGTGCTGCTGAGGAGAGATCTGTAGG 3441
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 Db 3442 GCAGAAAGGAGGCCAATACATACATGCTCTCATGAGTCACTGCTTAAATATATAGCACT 3501
 Qy 2524 CAAGTTGAGCTGAAGGAGCAGACGCTTCTGCGGCGCAGAAACAGACTAGCTATTGCA 2583
 Db 3502 AAAGTAGAGAAAGAACTCAGCTCTCTGTTGGCCAGAAACAGCAATTCGCCATAGCT 3561
 Qy 2584 AGGCTCTTCTCCAAAGCCCAAAATTTTATTTGATGAGGCGCCACTTCAGCCCTCGAT 2643

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 Db 3622 ACAGAAAGTGAAAGAGGTGTTCCAGAGGCCCCCTGGACAAAGCCAGAGAGGCCGACCTGC 3681
 Qy 2704 CTAGTGTCTACTCACAGGCTCTCTGCAATTCAGAAACGAGATTTGATAGTGTCTCTGCAC 2763
 Db 3682 ATTGTGATTGCTCACCGCTGTCCACATCCAGATGTCAGACTTATATAGTGTGTTTCAG 3741
 Qy 2764 AATGGAAGATTAAGGAAACAGGAACCTCATCAAGAGCTCTCTGAGAAATCGACATATAT 2823
 Db 3742 AATGGCAGAGTCAAGGAGCATGCGACGCGATCAGCAGCTCTGCGCACAGAAAGGCACTAT 3801
 Qy 2824 TTTAAGTTAGTGAATGCACAGTCCAG 2848
 Db 3802 TTTTCAATGTCAGTGTCCAGGCTG 3826

RESULT 15
 US-09-866-866A-3
 ; Sequence 3, Application US/09866866A
 ; Patent No. US20020102244A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sorrentino, Brian
 ; APPLICANT: Schuetz, John
 ; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
 ; FILE OF INVENTION: 1340-1-021CIP2
 ; CURRENT APPLICATION NUMBER: US/09/866,866A
 ; CURRENT FILING DATE: 2001-08-30
 ; PRIOR APPLICATION NUMBER: 09/584,586
 ; PRIOR FILING DATE: 2000-05-31
 ; PRIOR APPLICATION NUMBER: PCT/US99/11825
 ; PRIOR FILING DATE: 1999-05-27
 ; PRIOR APPLICATION NUMBER: 60/086,988
 ; PRIOR FILING DATE: 1998-05-28
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 3860
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-09-866-866A-3

Query Match 36.0%; Score 1028.6; DB 9; Length 3860;
 Best Local Similarity 62.2%; Pred. No. 9.8e-269;
 Matches 1694; Conservative 0; Mismatches 989; Indels 42; Gaps 3;

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Db 1462 ATTGCGTATGGCGTGAATAATGTCACCATGGATGAGATTGAGAAAGCTGTCAAGGAGGCC 1521
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QY 826 CGACTTCTACTATTCCAAAGTCAGATTTGATTTGTGACCCCTAAAGGATGAAATGCTGGCG 885
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Db 1882 ATGCGACAGCAGGAAATGAGTTGAAATGAGAAATGCACTGATGATCCAAAGTGAA 1941
QY 998 -----CTGAAGAGAGACCAACTCCTCTGCACTCTGTGCAAGAGATCA--- 1045
Db 1942 ATTGATGCCCTTGGAAATGCTCTCAATGATTCAGATCCAGTCTAATAGAAAGAGATCA 2001
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Db 2002 ACTGCTAGAGTGTCCGTGGATCACAAGCCCAAGCAGAAAGCTTAGTACAAAGAGGCT 2061
QY 1087 AAGAGATAAGTCTTCTGAGTCTCTATTAATAAATTTTAAAGTTTAAACAAGCCCTGAA 1146
Db 2062 CTGGATGAAAGTATACCTCCAGTTTCTTTTGGAGGATTTAGAGCTAAATTTAACTGAA 2121
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Db 2122 TGGCTTTTATTTGTTGTGTTGTTATTTGTGCAATTAATGAGGCTGCAACAGCA 2181
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QY 1504 GCAACAGTTCCAGATTTGGCTCTTAACCAAAATGCAATTAACATGAGGACTTTCAGTT 1563
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Db 2602 ATTGCAATAGCAGGAGTTTGTGAAATGAAATGTTTGTCTGGACAAGCACTGAAGATAAG 2661
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QY 1744 GTGTCAATTAACAGGGAAGAAAGCCTTCGAGCAAAATGATGAAAGAGATGTTTCAGACTCAA 1803
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QY 1804 CACAGAAATACCTCGAAGAAAGCACAGATTTATTGGAAGCTGTTATGCAATTCAGCCATGCC 1863
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Db 2842 ATGATGTAATTTTCTATGCTGATGTTTCCGGTTTGGAGCCTACTTGGTGGCACATAA 2901
QY 1924 CGAATGACCCAGAGGGCATGTTTCATAGTTTTCAGCAATTCGATATGAGCTATGGCC 1983
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QY 1984 ATCGGAAAAACGCTCGTTTGGCTCTGAAATATTCGAAAGCCAAATTCGGGGCTGGCCAT 2043
Db 2962 GTGGGCAAGTCAGTTCAATTTGCTCTGACTATGCCAAAGCCAAATATTCAGCAGCCAC 3021
QY 2044 CTGTTTGGCTTGTGGAAAAAGAAACCAATATAGACAGCCGCTCAGAAAGGAAAG 2103
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QY 2104 CCAGACACATGTGAAGGAAATTTAGAGTTTCAGAGAGTCTCTTCTTCTATCCATGCTGC 2163
Db 3082 CGAACACATTTGAGGAAATGTCACATTTGTTGAAGTTGTTTCACTATCCACCCGA 3141
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QY 2224 TTTTGGGAGCAGCGGCTGCGGAAAGACATTTCTGTTTCAACTTCTGACAGAGACTTTAT 2283
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QY 2464 GCGGCAATGACAGCAAAATATTCATTTTATTGAGGTTCTCCCTGAGAAATACACACA 2523
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QY 2524 CAAAGTTGACTGAAAGGAGCAGAGCTTTCTGGCGGCCAGAAAACAAAGACTAGCTATTGCA 2583
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QY 2584 AGGGCTCTTTCCAAAAACCCAAATTTTATTGTTGATGAGGCGCTCTTACGCCCTCGAT 2643
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Db 3622 ACAGAAAGTGAAGGTTTGTCCAGAAAGCCCTTGACAAAGCCCTGACAGAAAGGCGGACCTGC 3681

Qy	2704	CTAGTGGTCACACAGGCTCTCTGCAATTCAGAACCGAGATTTCGATAGTGGTTCTGCAC	2763
Db	3682	ATTGTGATGTCTACCGGCTGTCCACCATCCAGAAATGCAGACTTAATAGTGGTTTCAG	3741
Qy	2764	AATGGAAGATAAAGGAACAAGGAACCTCATCAAGAGCTTCCTGAGAAATCGAGACATATAT	2823
Db	3742	AATGGCAGATCAGGACGATGGCAGCATCAGCAGCTGCTGGCAGCAAGGATCTAT	3801
Qy	2824	TTTAAGTTAGTGAATGCACAGTCAG	2848
Db	3802	TTTTCAATGTCAGTGTCCAGGCTG	3826

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Job time : 1677 secs